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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
                                                                       Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Thetsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Contact: Shoemaker R/Public Soybean EST Project Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 14:1597-1604). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after inoculation and their mRNA pooled equally
and 53 hrs after insculation and their mRNA pooled equally
for cDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an XhoI restriction
site. EcoRI adaptors were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The CDNA insert is
protected from XhoI digestion via methylation during first
strand synthesis. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DHIOB host cells. Plant
care, inoculations, and library construction were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         performed by Steve Clough (Lila Vodkin lab, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
xhoI; The cDNA library was constructed from mRNA isolated
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/lab_host="DH10B"
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/clone_lib="Gm-c1074"
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                     AW761136 530 bp mRNA EST 21-NOV-2000 s163f12.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-6024 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
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Shoemaker,R., Keim,P.,
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first protected from XhoI digestion via methylation during first
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-/db_xref="taxon:3847"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="GENOME SYSTEMS CLONE ID: Gm-c1074-2145"
/clone_lib="Gm-c1074"
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Insert Length: 1680 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 420.
Location/Qualifiers
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XhoI; This cDNA library was constructed from mRNA isolution cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled
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seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-6024"
/clone_lib="Gm-c1027"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Coryell,V., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and Lewin,H. A Functional Genomics Program for Soybean (NSF 9872565)
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(217) 333-4582
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                                                                                                                                                                                                                                                                                                                                                                                                                   note="vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Library Gm-ri021 is a sequence-driven, reracked set of the original library Gm-ri04 which was prepared from root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cNNA. The Gm-c1004 library was constructed by Dr.
                                                                                     Center for Comparative and Functional University of Illinois,
                                                                                                                                                                                                                                    Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, AZ 86011 mail: paul.keim@nau.edu, virgill@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology Centers, University of Minnesota,
                            http://www.life.uiuc.edu/biotech/keck.html."
161 c 151 g 193 t 20 others
                                                                                                                                                  http://www.genomesystems.com,
                                                                                                                                                                                                           http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com.or
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sh75h06.y1 Gm-c1015 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1015-5652 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 1008 Std Error:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
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                                                                                                                                                        Erpelding.
                                                                                                                                                                                                      cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XIIO-Gold host cells. This library was constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                       XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt ended cDNA fragments followed by
                                                                                                                                                                                                                                                                                                                    XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                          XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5652"
/clone_lib="Gm-c1015"
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/db_xref="taxon:3847"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-6147
Fax: (217) 333-4582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Vodkin, L.O., PI, A Functional Genomics Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: AW432561 corresponding to Gm-c1015-5652 (5')
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
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GM700009B10H8
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Seq primer: 5'.TTTTTTTTTTTTTTTTTTT(A/C/G)-3'.
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  D
                                                                                                                                                                                                                                                                                                                                                                                                       various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-r1070. The CDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The
                                information on the source library for each clone can also
be obtained by referring to the Genome Systems clone ID of
the original cDNA library that is also listed under
'OTHER EST'."
                                                                                                                        http://www.life.uiuc.edu/biotech/keck.html. Note: Tocresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The det
                                                                                                                                                                                                                              Reracking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Keck Center for Comparative and Functional Genomics.
                                                                                                                                                                                                                                                                                                                                    contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Center for Computational Genomics and Bioinformatics, University of Minnesota,
                                                                                                                                                                                                         University of Illinois,
                                                                                                                                                                                                                                                                                                            http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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/note="The library Gm·r1070 is a sequence-driven,
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/clone="Gm-r1070-3447"
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                                                                                                                              The detailed
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Location/Qualifiers
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HS_5183_Al_B08_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=759 Col=15 Row=C, DNA sequence.
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Class: BAC ends
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Plate: 759 row: C column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 Queen Anne Avenue North, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High Throughput Sequencing Center University of Washington
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 616-3618
(206) 616-3887
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                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen do and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

3 79 c 86 g 101 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Plate=759 Col=15 Row=C"
/clone_lib="RPCI-11 Human Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.1%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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0.0011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Male BAC Library"
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                                                                                                                                                                                                                                                                     GTATTGTAAATGTGAGATGCC 436
AW586761 514 bp mRNA EST 07-SEP-2000 EST318384 MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone pMHAM-55G12, mRNA sequence. AW586761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE999004
EST430727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://chrysie.tamu.edu/medicago
Seg primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M272982e TIGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P., Town,C.D., Bowman,C.L., Craven,M.B., Cho,J. and Fraser,C.M. ESTs from senescent nodules of Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolieae;
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BE999004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicago truncatula
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note-"Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GVSN"
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/cultivar="genotype_A17"
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sequence

name:

St.Paul, MN 55108 USA

COMMENT

MEDLINE JOURNAL TITLE REFERENCE

AUTHORS

SOURCE KEYWORDS

ORGANISM

DEFINITION AQ451805/c LOCUS RESULT

ACCESSION

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                               BF650924 539 bp mRNA EST 20-DEC-2000 NF098E01EC1F1005 Elicited cell culture Medicago truncatula cDNA clone NF098E01EC 5', mRNA sequence.
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The Samuel Roberts Noble Foundation
ON 73401, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula/Glomus versiforme mixed EST library. Medicago truncatula/Glomus versiforme mixed EST library Eukaryota; mixed EST libraries.
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BF650924.1
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Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M. ESTs from roots of Medicago truncatula after colonization with
                                                               Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Maria J. Harrison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Torres-Jerez, I.,
                                                                                                                                                             barrel medic
                                                                                                                                                                                     EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mjharrison@noble.org
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                   (bases 1 to 539)
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580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
/dev_stage="Roots harvested at 10, 122, 31 and 38 days
/dev_stage="Roots harvested at 10, 122, 31 and 38 days
/sost-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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library"
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/clone="рмнам-55G12"
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Scott, A.D.,
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Pred. No.
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Harris, A.R.,
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Gonzales, R.A.,
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                                                                      Trifolieae
Bell, C.J.
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Best Local
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                                Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle,
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name:M261621e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BE124753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: radixon@noble.org
Insert Length: 539 Std Error: 0.0
Plate: 098 row: E column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
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Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST393788 GVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
                                                                                                                                                                                        Unpublished (2000)
                                                                                                                                                                                                                                                                      Fedorova,M., Pierson,B.L.,
,H., Ellis,L., Town,C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                            barrel medic
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                TIGR sequence name:MTCCC28TK
                                                                                                                                                                                                              truncatula
                                                                                                                                                                                                                                ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                    Holt, I.E. and Fraser, C.M
More information is
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1. .539
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/db_xref="taxon:3880"
/clone="NF098E01EC"
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Pred. No.
                                                                                                                Upper Buford Circle,
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BE997991.1
EST.
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                                                                                                                                                                            Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M271969e TIGR sequence
MTKAK29TK More information is available at:
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                               411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Carroll P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                Department of Agronomy and Plant Genetics University of Minnesota
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Location/Qualifiers
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1014 c 137 g 167 t 1 others
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/dev_stage="effective root nodules harvested one month
post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; CDNA was prepared from polyA+ enriched RNA from
effective root nodules harvested one month post
inoculation with Sinorhizobium meliloti. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
ctatters and sinorhizobium the Uni-ZAP XR vector from
                                                                  /cultivar="genotype A
/db_xref="taxon:3880"
/clone="pGVSN-8F9"
/tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from
                                                /clone_lib="GVSN"
                                                                                                                                /organism="Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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Pred. No.
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Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed Eukaryota; mixed EST libraries.

[ (bases 1 to 635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            available at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other name: MHAM-7a-F10; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mjharrison@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Harrison M.J.
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21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from roots of Medicago truncatula after colonization with
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host-"E. coli strain XLOLR"
/note="Yector: pBluescript SK"; Site_1: EcoRI: Site_2:
XhoI: cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/lab_host="E. coli strain SOLR"
/note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhOI; CDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP ZR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing CDNA inserts were excised from the recombinant lambda-ZAP phage-using Ex-Assist helper phage and propagated in SOLR cells."

58 a 114 c 143 g 171 t
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:119092"
/clone="MHAM-7K19"
                                                                                                                                                                                                                                                                                      /clone_lib="MHAM"
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                                                                                                                                                                                                                                                                                                                                                            /cultivar="Medicago truncatula genotype A17"
                                                                                                                                                                                                                                                                                                                                                                                                          organism="Medicago truncatula/Glomus versiforme mixed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mjharrison@noble.org
Other name: MHAM-7a-F11; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrysie.tamu.edu/medicago'.
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h 17.1%; Score 21;
Similarity 100.0%; Pred. No.
21; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Samuel Roberts Noble Foundation
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580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     580-221-7380
                                                                                                                             /lab_host="E. Coli strain XIOLR"

/note="Vector: pBluescript SK-; Site_1: Econ; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 day: post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
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159 c 103 g 171 t
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/db_xref="taxon:119092"
/clone="MHAM-7K21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Medicago truncatula/Glomus versiforme mixed EST library"
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RESULT 16
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AW584948/c
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AQ597145 444 bp
HS_5240_A1_B11_SP6E
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Other name: MHAM-7d-E06; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tays (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed EURaryota; mixed EST libraries.
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Fax: 580-221-7380
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Contact: Harrison M.J.
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                                                                                                                                                                                                                                                                                                                                                              /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
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100.0%;
    P DNA
RPCI-11 Human Male
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                                                                                                                                                                                                                                                        Score 21;
Pred. No.
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                                                                                                                                                                                                                                                                             Length 682;
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DEFINITION

BAC Library

sapiens

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                        AUTHORS
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                                                                                                                                                                                                                                                                                                               47
                                                                                                                                                                                                                                                                                                                                              98 ttatcttcaatttattcc 115
                                                                                                                                                                                                                                                                                                             TTATCTTCAATTTATTCC
                                                                                                                                                                            BE653345 468 bp mRNA EST 06-9 UI-M-AL1-ahi-c-07-0-UI.rl NIH_BMAP_MCO_N Mus musculus UI-M-AL1-ahi-c-07-0-UI 5', mRNA sequence.
                    1 (bases 1 to 468)
Bonaldo, M.F., Lenno
                                                                                                                                                 BE653345.1
Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                           Mus musculus
                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                             house mouse
                                                                                                                                                                   BE653345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 816 row: C column: 21
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401 Queen Anne Avenue North, Seattle, WA 98109,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mahairas GG, Wallace JC, High Throughput Sequencing Center University of Washington
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Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mahairas, G.G.,
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Mammalia; Eutheria;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"

96 c 103 g 131 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=816 Col=21 Row=C"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                 GI:9979245
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Primates;
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Pred. No.
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                                                     Euteleostomi;
; Murinae; Mus
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AQ597171/c
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MEDLINE
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Best Local
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AQ597171.1
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56 gagggctgcactgactgg 73
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                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ597171 487 bp DNA GSS 08-JUN-1999 HS_5240_Al_El2_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=816 Col=23 Row=I, DNA sequence.
                                                                    High Throughput Sequencing Center University of Washington
                                                                                                                                                              Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 487)
Mahairas, G.G., Wallace, J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              discovery
Genome Res. 6 (9),
97044477
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20892-9643, USA
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                                                                                                                                                                                                                                                                                                                                                                                                             Keller,A., Shaker,R., Furlong,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               availability will be considered under appropriate and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mEST@mail.nih.gov
Queen Anne Avenue
: (206) 616-3618
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301 443 9890
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/dev_stage="27-32 days"
/lab_host="PHIOB (Life Technologies)"
/lab_host="PHIOB (Life Technologies)"
/lab_host="FIOT3D-Pac (Pharmacia) with a modified
/note="Vector: pTTT3D-Pac (Pharmacia) with a modified
polyllnker; Site_1: Not I; Site_2: Eco RI; The
notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Notyllnker; Site_1: Not I; Site_3: Eco RI; The
// Not I; Site_3: Ec
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Tissue provided by Ms. Annie Novakovich,
rahoratories."
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/clone="UI-M-AL1-ah1-c-07-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:5028383
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100.0%;
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Pred. No.
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                                      North,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                      Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, K.,
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23;
                                                                                                                                                                  Hood
                                                                                                                                                                                                                                                                                                                                                                                                         Young, J.,
                                          WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                             Swartzell,S.,
g,J., Zhao,S.,
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                                                                                    Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.tlgr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 337 row: C column: 12
                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BH054207 533 bp DNA GSS 17-RPCI-24-337C12.TJ RPCI-24 Mus musculus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Other_GSSs: RPCI-24-337C12.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 533)
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Location/Qualifiers
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                                          Class: BAC ends
                                                                                                                                                                                                                                                           9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH054207.1 GI:14849018
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Plate: 816 row: I column: 23
                                                                   Seq primer: SP6
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Email: jwallace@u.washington.edu
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                                                                                                                                                                                                                                                                                                                                Institute for Genomic Research
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                                                                                                                                                                                                                                  szhao@tigr.org
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                 Location/Qualifiers
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/clone="Plate=816 Col=23 Row=I"
/clone_lib="RPCI-11 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                                                                                                                                                 http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 129 row: H column: 21
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Other_GSSs: RPCI-23-129H21.TJ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
DNA."
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size
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/clone="RPCI-24-337C12"
/clone_lib="RPCI-24"
                                                                                                          /clone_lib="RPCI-23"
/sex="Female"
                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-129H21"
                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                      /organism="Mus musculus"
                                                                                                                                                                                                                                                             Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 tcttcaatttattccaca 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Fraser,C.M.

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-34A15.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 34 row: A column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ243191 595 bp DNA GSS 15-JUN-2000 RPCI-23-34A15.TV RPCI-23 Mus musculus genomic clone RPCI-23-34A15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao, S., Nierman, W., Feldblyum, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                  Conte-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="RPCI-23-34A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                   /sex="Female"
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24;
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23;
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BF815581/c
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AZ396970 606 bp .DNA GSS 03-OCT-2 1M0161D13R Mouse 10kb plasmid UUGC1M.library Mus musculus
                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: puc 18 forward High quality sequence stop: 599.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-MR2&t2-MR2-CI0128-041200-009-c02&t3=2000-12-04&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,F.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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+55-11-2707001
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                                                                                                                                                                                                                                                                                                                  /note="Organ: colon_ins; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

a 137 c 151 g 152 t 3 others
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/clone_lib="CI0128"
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BF208765
                                                                                                                                                                                18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0161 row: D column: 13 seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
High quality sequence stop: 606.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mmalia; Eutheria;
(bases 1 to 606)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308,
                                                                                                                                                                                                                                                                                                           147
                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114 gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and provided to adaptors and sheared. Adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                         adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

95 c 107 g 257 t
                                                                                                                                                                                                                                                                                                                                                                                   purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jack Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
/clone="UUGC1M0161D13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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606
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                                                                                                                                                                                                   Score 18;
Pred. No.
  mRNA
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24;
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; Murinae; Mus
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AV326766
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                                                                                                                    AUTHORS
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1 (bases 1 to 634)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         601872235F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:4093065 5',
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. 1 (bases 1 to 167)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Frukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Co, Kawai, J., Kaikuchi, N., Kajima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
                                                                                                                                                                                                                                                                                                                                                AV326766 167 bp mRNA EST 11-NOV-1999
AV326766 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330415D21 3', mRNA sequence.
AV326766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BF208765
BF208765.1 GI:11102351
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                               house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="carcinoma, cell line"
/tlssue_type="carcinoma, cell line"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/note="Organ: bladder; Vector: pDNR-LIB (Clontech);
/site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Site_1: SfiI (ggccgctcggcc); Site_2: SfiI (ggccattatggcc);
Duble-stranded cDNA was prepared from cell line RNA.
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAAAGGCCGACATG-dT(30)BN-3'
(where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.55 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

84 a 176 c 165 g 109 t
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/clone_lib="NIH_MGC_53"
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/db_xref="taxon:9606"
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Pred. No.
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                    28 caaccctgatgacctaa 44
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CAACCCTGATGACCTAA 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sughiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y. and Hayashizaki,Y.
                                                                                                                                                                                                               58
                                                                                  Conservative
                                                                                                                                                                                                               Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                               3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                       BamHI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="6330415D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="medulla oblongata"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, adult male medulla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                  13.8%;
                                                                                                                                                                                                             42 c
                                                                                0;
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Pred. No.
                                                                                                                                                                                                          31 g
                                                                                  Mismatches
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74;
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                                                                        AV337137 249 bp mkww
AV337137 RIKEN full-length enriched,
AV337137 cDNA clone 6332414J18 3
                                                                                                                                                                                                                                                                             l Similarity
17; Conserv
Mus musculus
                                                 AV337137.1
                                                                     Mus musculus
AV337137
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Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 202.
Location/Qualifiers
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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                nouse mouse.
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(bases 1 to 211)
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="mAGE:1262011"
/clone_lib="Stratagene mouse skin (#937313)"
/sex="females"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="ll weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole skin"
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/strain="C57BL/6"
                                                 GI:6377189
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Rodentia;
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Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki v and Hawashizaki v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High-efficiency full-length cDNA cloning. Methods Enzymol. 19-44 (1999)
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Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                          prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                        prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="0332414J18"
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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RIKEN Mouse ESTs (Konno, H., et al.)
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jap
Tel: 81-45-503-9222
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Contact: Yoshihide Hayashizaki
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
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19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            system.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Carninci,P. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y. and Hayashizaki,Y.
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/note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike
                                                                                                                                                                           cerebellum"
                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="C230019C09"
                                                                                          /dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                /tissue_type="cerebellum"
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
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Research Group in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RS KONNO, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishi, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACCCTGATGACCTAA 151
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                                                  Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
                                                                                                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazak:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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AV277980
                                                                                                                                                                                                                                                                                         Matsuura, S., Carninci, P., Muramatsu, M.,
                                                                                                                                                                                                                                                                                                                 Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., (
                                                                                                                                                                                                                                                                                                                                                                                                                                         1-7-22 Suehiro-cho,
Tel: 81-45-503-9222
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
                                Carninci, P. and Hayashizaki, Y.
                                                                                                                    Y. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                   Ozawa,K., Tanaka,T., Yoneda,Y.,
su,M., Okazaki,Y. and Hayashizaki
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M., Okazaki
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                                                                                                                            Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M. Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Satai, C., Sato, K., Shibata, Y., Shigamoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Yamamura, T., Yamanaka, I., Tagawa, A., Watanabe, S., Yamamura, T., Yamanaka, I., Watanabe, S., Yamamura, T., Yamanaka, I., Watanabe, S., Yamamura, Yamanaka, I., Yamanaka, I., Watanabe, S., Yamamura, Yamanaka, I., Watanabe, S., Yamamura, Yamanaka, I., Yamanaka, I., Watanabe, S., Yamamura, Yamanaka, I., Yamanaka, I., Watanabe, S., Yamamura, Yamanaka, I., Yamanaka, Yamanaka
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BB248570
                             ,M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
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Mammalia; Eutheria;
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                                                                                                   Yano, R., Yasunishi, A., Yokota, T., Yoshida, K.,
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
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                                                              AI466360 301 bp mrNA
vw88b10.y1 Stratagene mouse skin
IMAGE:1262011 5', mRNA sequence.
                                                                                                                                                                                                                                                                          l Similarity
17; Conser
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                      AI466360.1
                                                         AI466360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y.
 house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sciences Center(GSC), Yokohama Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-44 (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High-efficiency full-length cDNA cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                       modified pBluescript KS(+) after bulk excision from Lambda FLC I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research output in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerebellum"
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/lab_host="DH10B"
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/dev_stage="7 days neonat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RIKEN full-length enriched, 7 days neonate
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                                                                                                                                                                                               sequence.
BI188737
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                                                                                                                                            Fusarium sporotrichioides.
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Marra, M., Hillier, L.,
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ORGANISM
Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A.,,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                             BI188737 316 bp mRNA EST 10-JUL-2001 d2g04fs.rl Fusarium sporotrichioides Tri 10 overexpressed cDN library Fusarium sporotrichioides cDNA clone d2g04fs 5', mRNA
                                                                                                                                                                            Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                 Hypocreales; mitosporic Hypocreales;
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR (kanamycin resistant)"
/note="Organ: skin; Vector: pBluescript SK:; Site_1: EcoRI
/note="Organ: skin; Vector: pBluescript SK:; Site_1: Cligo
dT. Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'
adaptor sequence: 5' GAGTTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="whole skin"
/dev_stage="11 weeks old"
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/clone="IMAGE:1262011"
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/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI266425 329 bp mRNA EST 18-JUL-2001 NF097C04IN1F1034 Insect herbivory Medicago truncatula cDNA clone NF097C04IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Korth K
                                                                                                                                                                               University of Arkansas
217 Plant Science Building,
Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                   Dept. of Plant Pathology
                                                                                                                                                                                                                                                                                                         Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A.,
H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts No
Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
84 0.072 gil5668770|gb|AAD459 (AC005916) T17H3.9
                                                                                                       Email: kkorth@comp.uark.edu
Insert Length: 329 Std Error: 0.00
Plate: 097 row: C column: 04
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 136
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
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               /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF097C04IN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pBlueScript SK-; Site_1: EcoRI; Site_2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript; 3' end of cDNA cloned into XhoI site of pBluescript" 102 c 63 g 69 t
/clone_lib="Insect herbivory"
                                                                                        Location/Qualifiers
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/clone="d2g04fs"
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/strain="Tri 10"
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nc06c06.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1007338
similar to contains Alu repetitive element;contains element MER35
repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 334)
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                                                 /note="Vector: pamp10; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(d7)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10 ,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pamp10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by
                             David Krizman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

1 2 others
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/dev_stage="mature"
/note="vector: Lambda Zap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                    /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1007338"
                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Pr1"
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C70635 Yuji Kohara unput
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                                       Medicago truncatula
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                   BI266362 366 bp mRNA EST MR092D09IN1F1078 Insect herbivory Medicago NF092D09IN 5', mRNA sequence.
                                                                                                                 EST.
  1 (bases 1 to 366)
Korth, K., Scott, A.D
                                                                                                                              BI266362.1 GI:14870403
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Caenorhabditis elegans
                                Medicago
                                                                                                    barrel medic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     National Institute of Genetics
Yata 1111, Mishima, Shizuoka 4
Tel: 81-559-81-6854
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Yuji Kohara
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Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H.,
_M., Miyata,A. and Nishigaki,A.
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                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Yuji Kohara unpublished /sex="hermaphrodite, male" /tissue_type="whole animal" /dev_stage="varied" 10 t 10 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
  Scott, A.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="yk411b1"
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 Harris, A.R.,
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Pred. No.
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78;
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79;
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Gonzales, R.A.,
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truncatula cDNA clone
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Bell, C.J., Flores
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              The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized corpus striatum library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
                                                                                                                                                                                                                                                                                                                                                         Bonaldo, M.F., Lenno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW457639 450 bp mRNA EST UI-M-BH3-ari-a-04-0-UI.S1 NIH_BMAP_M_S4 Mus UI-M-BH3-ari-a-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
17; Conserv
clones from RESEARCH GENETICS.
                                                                                                                                                                      Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                              National Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC
                                                                                                                                                                                                                                                                                                         Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                               discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: kkorth@comp.uark.edu
Insert Length: 366 Std Error: 0.0
Plate: 092 row: D column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
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217 Plant Science Building,
Tel: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                              20892-9643, USA
                                                                                                                                                                                                                            6001 Executive Blvd. Room
                                                                                                                                                                                                                                                                       Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                               Normalization and subtraction:
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Contact: Korth K
                                                                                                                                                    Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula insect herbivory library
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expanded M. truncatula leaves of plants fed upon by spodoptera exigua (beet armyorm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled. 9
69 c 52 g 128 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Zap; Library was produced from fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="local and systemic leaves"
/dev_stage="mature"
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/db_xref="taxon:3880"
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                                                                                                                                          Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzale Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
                                                                                                                                                                                                                                                                                                                              EST
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Seq primer: w13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                       (bases 1 to 456)
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TAG_SEQ=ACGGC"
109 g 104 i
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/clone="UI-M-BH3-ari-a-04-0-UI"
/clone_lib="NIH_BMAP_M_S4"
/clone_lib="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B_(Life_Technologies)"
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                                                                                                                                                                                                                                       Voyata, H
Contact: Chin, H
National Institute of Mental Health
National Institute of Mental Health
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UI-M-BZ1-bft-e-20-0-UI.sl NIH_BMAP_MHI2_Sl Mus musculus cDNA clone UI-M-BZ1-bft-e-20-0-UI 3', mRNA sequence.
               The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to verify it as a clone from the hippocampus tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH
                                                                                                                                                             Tel: 301 443 1706
Fax: 301 443 9890
Email: mEST@mail.nih.gov
                                                                                                                                                                                                                            6001 Executive Blvd. 20892-9643, USA
                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                       discovery
                                                                                                                                                                                                                                                                                                                                                                                            Bonaldo, M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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Seq primer: TCACACAGGAAACAGCTATGAC.
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Dixon RA
GENETICS. It should be noted that Bento Soares is
                                                                                                                                                                                                                                                                                                                                                                      Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE989827.1
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                                                                                                                                                                                                                                                                                                                                                                                                                 (bases
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/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
/note="Vector: Lambda Zap; Cells were induced with yeast
cell wall extracts equivalent to 50ug/ml glucose in the
final concentration. Samples were taken at 0.5, 1, 12 an
24 hours after induction. Equal amounts of RNA from each
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF082D01EC"
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1. .456
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Pred. No.
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BASE COUNT
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AUTHORS
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                                                                                                                                                                              Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 519)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Thising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurt,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW394535 519 bp mRNA EST 07-FEB-2000 sh32c05.yl Gm-c1017 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1017-3393 5' similar to TR:O83191 O83191 CONSERVED HYPOTHETICAL
This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN. ;, mRNA sequence.
AW394535
AW394535.1 GI:6912947
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                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycine max
                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soybean.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.

TAG_LIB-NIH_BMAP_MHI2_S1

TAG_TISSUE-hippocampus

TAG_TISSUE-hippocampus
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_MHIZ_S1 library is a subtracted library derived from NIH_BMAP_MHIZ_NIH_BMAP_MHIZ is a library derived from NIH_BMAP_MHIZ. NIH_BMAP_MHIZ is a library derived from NIH_BMAP_MHIZ.
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/db_xref="taxon:10090"
/clone="UI-M-BZ1-bft-e-20-0-UI"
/clone_1lb="NIH_BMAP_MHIZ_S1"
/dev_stage="27-32 days"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ626769 526 bp DNA GSS 13-DEC-1M0467008F Mouse 10kb plasmid UUGCIM library Mus musculus clone UUGCIM0467008 F, DNA sequence.
                                                                                                                                                                                                                        Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0467 row: O column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            University of Utah
University of Utah
                                                                      High quality sequence stop: 526.
Location/Qualifiers
                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                        Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
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High quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biomedical Polymers Research Bldg.,
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/organism="Mus musculus"
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/clone_lib="Gm-c1017"
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/lab_host="XL10-Gold"
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/db_xref="taxon:3847"
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17; Conserv
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OV1_14_H02.g2_A002
                                                                                                                                                                            Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                                                                                                                                                                                                                                                                   The University of Georgia
Plant Sciences Building, Rm. 2502, Athens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                      Contact: Cordonnier-Pratt MM
Department of Botany
                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              An EST database from Sorghum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sorghum bicolor
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                                                                                            High quality sequence start: 30 High quality sequence stop: 541
                                                                                                                                                primer: PolyTMix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

97 c 92 g 122 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732141 gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                 Location/Qualifiers
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musculus C57BL/6J (male) was obtained fr
/organism="Sorghum bicolor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Mouse 10kb plasmid UUGC1M library"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erry
Plate: 0229 row: L column: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: CACACAGGAAACAGCTATGACC Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2M0229L22R Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0229L22 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid inserts
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                  was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                      /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biomedical
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                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0229L22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Ovary 1 (OV1)"
/note="Organ: Mix of ovaries of varying immature stages from 8-week-old plants; Vector: pBluescript II from Lambda gap II; Site_1: XhoI; Site_2: EcoRI; The library was made
10.5 kb range using preparative agarose gel
                                                                                                                                                  (http://www.jax.org/resources/documents/dnares/). The DNA
                                                                                                                                                                                                                                        /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                /sex="Female"
                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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100.0%; Pr
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             actggtaagtttcacat 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: RPCI-23-21704.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 217 row: O column: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Institute for Genomic Research 9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse BAC End Sequences from Library RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao,S., Nierman,W., Feldblyum,T., Malek,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
l (bases 1 to 555)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ561989.1 GI:11241809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                              BAC ends.
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/GJ mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "108 c 116 g 138 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                              /clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="RPCI-23-21704"
                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                           'lab_host="DH10B"
                                                                                                                                                                                                                     'sex="Female"
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Pred. No.
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                             5 tattgtaaatgtgagat 21
                                                                                                                                                                                                                                                                                               High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              Seq primer: T7
Class: BAC ends
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California Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A sea urchin genome project: Sequence scan, virtual map, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ149056 28-AUG-2000 ASS 28-AUG-2000 SP_0046_A1_B09_T7 Strongylocentrotus purpuratus, purpule sea urch sperm genomic BAC library Strongylocentrotus purpuratus genomic clone_Plate=46 Col=17 Row=C, DNA sequence.
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                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                            Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                           Pasadena California 91125,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cameron,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strongylocentrotidae; Strongylocentrotus.
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(626) 793-3047
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/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
                                                                                                                                                                                   /note="Organ:
                                                                                                                                                                                                                                                    /db_xref="taxon:7668"
                                                                                                                                                                                                                                                                 organism="Strongylocentrotus purpuratus"
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Pred. No.
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SUMMARIES

<i>:</i>			TITLE JOURNAL COMMENT
* 13276 * 14179 * 15073 * 15955 * 16817 * 17751 * 18614 * 19491	* 5298 * 6184 * 7058 * 7990 * 8860 * 9722 * 10594 * 11473 * 11382	http://ftp.genome.w. *NOTE: This record *sequencing reads *contigs. Runs of *and the order in *arbitrary. Low-pa: *identifying clone: *overlap relations *however, it shoul. *will be sequenced *the record is upd *be preserved. 934 1798 2684 3570 4443 *4444 5297	Ferreira, P., FitzHugh, Galagan, J., Gardyna, S., Howland, J.C., Johnson, Lehoczky, J., Lieu, C., McEwan, P., McGurk, A., Morrow, J., Naylor, J., Peterson, K., Pollara, V. Stange-Thomann, N., Storestaye, S., Tirrell, A., Tesfaye, S., Tirrell, A., Wyman, D., Ye, W. J., Zin, Direct Submission Submitted (28-SEP-1995 Research, 320 Charles all repeats were idented and the state of the
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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Kara-Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J
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                                              Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham
                                                                                                                                                               Homo sapiens, clone RP11-22D13
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldarim, J., Menga, V., Morrow, J., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani, C., Pisani, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani, C., Riley, R., Rogov, P., Rothman, D., Rogov, P., Rothman, P., Rogov, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Jun 4, 2000 this sequence version replaced gi:7798779. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996–1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                              1212: contig of 1212 bp in length
1213 1312: gap of 100 bp
1313 5818: contig of 4506 bp in length
5819 5918: gap of 100 bp
5919 9462: contig of 3544 bp in length
9463 9562: gap of 100 bp
9563 15211: contig of 5649 bp in length
15212 15311: gap of 100 bp
15312 28255: contig of 12944 bp in length
28356 28355: gap of 100 bp
28356 44646: contig of 16291 bp in length
44647 44746: gap of 100 bp
44747 63409: contig of 18663 bp in length
145845 145944: (
145945 178035)
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Consensus quality: 169315 bases at least Q40
Consensus quality: 173915 bases at least Q30
Consensus quality: 175957 bases at least Q20
Insert size: 170000; aggarose-fp
Insert size: 177035; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
Quality coverage: 4.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                              63410 63509:
63510 9049
90495 90594:
90595 11852
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118630 14584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
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                                                                                     63509: gap of 100 bp in 1.
90494: contig of 26985 bp in 1.
90594: gap of 100 bp
118529: contig of 27935 bp in 1.
118629: gap of 100 bp
145844: contig of 27215 bp in 1.
     178035: cont
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/organism="Homo sapiens" /db_xref="taxon:9606"

/clone="RP11-22D13"

/clone_lib="RPCI-11 Human Male BAC'

Location/Qualifiers

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Best Local (
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                                                                                                                                                                                                                                                                           Bruce, D., Mundt, M., Dóggett, N., Munk, C., Saunders, E., Robinson, D., Jones, M., Buckingham, J., Chasteen, L., Thompson, S., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmire, J., White, S., Tatum, O., Campbell, C., Fawcett, J., Maltbie, M., Bussod, M., Sutherland, R., McMurry, K., Han, C. and Deaven, L.
                                                                                   Sequence Quality Assessment:
This entry has been annotated with sequence quality
estimates computed by the Phrap assembly program.
All manually edited bases have been reduced to quality zero.
                                                                                                                                                                              Genome Institute, Los Alamos National Laboratory, MS M888, Alamos, NM 87545, USA On Jul 3, 2001 this sequence version replaced gi:8575868.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC007600 183079 bp DNA HTG 03-JUL-20 HOMO Sapiens chromosome 16 clone RP11-264A16, WORKING DRAFT
                                                                                                                                                                                                                                                      Submitted (20-MAY-1999) Center for Human Genome Studies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 183079)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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AC007600.4 GI:14589421
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                                             Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
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90595. .118529
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AL Unpublished.

AL Unpublished.

Diases I to 194198)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Boguslawkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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Birren, B., Linton, L.,

Homo sapiens, clone RP11-3N3

Homo sapiens

AC013298.6 HTG; HTGS_F

HTGS_PHASE1; HTGS_DRAFT

GI:10198404

pieces

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194198)

Nusbaum, C. and Lander, E

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Query Match
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Homo sapiens clone
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This entry has been annotated with sequence quality
This entry has been annotated by the Phrap assembly program.
All manually edited bases have been reduced to quality
                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of this entry's ASN.1 file.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality levels above 40 are expected to have less than 1 error in 10,000 bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 183079: contig of 183079 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces \frac{1}{2}
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .183079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16"
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-264A16"
41752 c 42357 g 51492
194198 bp DNA HTG 20-SEP-2000 ns clone RP11-3N3, WORKING DRAFT SEQUENCE, 19 unordered
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Pred. No.
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0.31;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 185739 bases at least Q40
Consensus quality: 185725 bases at least Q30
Consensus quality: 191725 bases at least Q20
Insert size: 194000; agarose-fp
Insert size: 194000; agarose-fp
Quality coverage: 5.4 in Q20 bases; agarose-fp
Quality coverage: 5.5 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                              58724 58823: gap of 100 bp 58824 68160: contig of 9337 bp in length 68161 68260: gap of 100 bp 68261 84475: contig of 16215 bp in length 84476 84575: gap of 100 bp 84576 98534: contig of 13959 bp in length 98535 98634: gap of 100 bp 98535 114643: contig of 16009 bp in length 98535 114643: contig of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 .10747: contig of 16747 bp in length
16748 16847: gap of 100 bp
16848 18184: contig of 1337 bp in length
18185 18204: gap of 100 bp
18205 21234: contig of 2950 bp in length
21235 21334: gap of 100 bp
21335 23349: gap of 100 bp
23493 23592: gap of 100 bp
23593 26852: contig of 3260 bp in length
26853 26952: gap of 100 bp
26853 36957: contig of 3260 bp in length
26853 36957: contig of 3925 bp in length
                                                                                                             114644 114743: gap of 100 bp
114744 144676: contig of 29933 b
144677 144776: gap of 100 bp
144777 160047: contig of 15271 b
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Contact: sequence_submissions@genome.wi.mit.edu
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10970: contig of 4893 l
15970: gap of 100 1
791
                        8936: gap of
194198: cont
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178836: contig of 18689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                  004: gap of 100 bp
51760: contig of 6756 k
360: gap of 100 bp
58723: contig of 6863 k
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contig of 4721 h
                  contig of 15262 bp in length
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RESULT 5
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                                                                                                                    AP000958 50974 bp DNA PRI 14-JAN-2000 Homo sapiens genomic DNA, chromosome 21q21.1-q21.2 clone:B794P4, LL56-APP region, complete sequence.
                                            Homo sapiens DNA, clone:B794P4 Homo sapiens
                                                                                                                                                                                                                                                                                            21;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 50974)
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84576. .98534
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment
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|14744. .144676
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58261. .84475
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Direct Submission
Submitted (01-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Sep 1, 2000 this sequence.
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The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 155304)
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1 (bases 1 to 155304)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 50,974 genomic DNA of 21q21.1-q21.2 Published Only in DataBase (1999) In press 2 (bases 1 to 50974)
                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Ishii,K.,
Fujiyama,A., Yada,T.,
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                                                                                                                                       site:http://genome.wustl.edu/gsc/index.shtml
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Consensus quality: 142506 bases at least Q30 Consensus quality: 144038 bases at least Q20 Insert size: 150000; agarose-fp Insert size: 150578; sum-of-contigs Quality coverage: 3.56 in Q20 bases; agarose-fp Quality coverage: 3.67 in Q20 bases; sum-of-contigs
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                                               /note="assembly_name:Contig43"
134509. .155304
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69839. .76434
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                                                                                 122093
                                                                                               note="assembly_name:Contig42"
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                                                                                                                             note="assembly_name:Contig41"
                                                                                                                                                           /note="assembly_name:Contig40"
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45231. .49657
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37143. .40035
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                                                                                                                                                                                                                                                                                                                                                                                                                                         note="assembly_name:Contig32"
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/db_xref="taxon:9606"
/chromosome="21"
                                                                                                                                                                                                                                                                  'note="assembly_name:Contig37"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig28"
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L927. .3373
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            embly_name:Contig44"
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                                                                                                  The following BAC sequence is oriented from the T7 to the SP6 end. IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage, etc. . even if efforts are made to eliminate these contaminating sequences.
                    UNSUTEFA 158927 bp DNA HTG
Homo sapiens chromosome 14 clone R-326E7, ***
PROGRESS ***, 2 ordered pieces.
AL512361
Assembly program: Phrap; version 2.0
Quality coverage: 5.91x in Q20 bases; sum-of-contigs

    Web: www.genoscope.cns.fr)
    On Apr 4, 2001 this sequence version replaced gi:11990876

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Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Winck Brottlier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguena Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J. Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                  Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                          Percentage of bases with a quality value >=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (29-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HTG; HTGS_F
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PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT
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Eukaryoʻta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 171345)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletter,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Gyapay,G., Saurin,W. and Weissenbach,J.

Sequencing of the human chromosome 14
                                                                                                                                                                                                                                                                                                         CNS01RII 171345 bp DNA PRI 28-APR-2001
Human chromosome 14 DNA sequence BAC R-346L24 of library RPCI-11
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60765 bp contig from 98163 to 158927.

* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                             Homo sapiens
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1 98062: contig of 98062 bp in length
98063 98162: gap of 100 bp
98163 158927: contig of 60765 bp in length.
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//note="matching EMBL:Z23897
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 182340)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-221C21

    Web: www.genoscope.cns.fr)
    On Mar 12, 2001 this sequence version replaced gi:11875958.
    ----- Genome Center

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-326E7 Downstream BAC (overlapping the SP6 end): R-649E7 (AC-AL139099)

The following BAC (overlapping the SP6 end): R-649E7 (AC-AL139099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-APR-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                    Homo sapiens
                                                                                                                                        AC024417.2 GI:7229920
HTG; HTGS_PHASE1.
                                                                                                                                                                                                  ACO24417 182340 bp DNA HTG
Homo sapiens chromosome 4 clone RP11-221C21
IN PROGRESS ***, 64 unordered pieces.
                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                        AC024417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Overall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Assembly program: Phrap; version 2.0 Quality coverage: 9.09x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Genoscope / Centre National de Center code: GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genoscope.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percentage of bases with a quality value >=
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 171345)
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quality chart :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="R-346L24"
/clone_lib="RPCI-11"
35560 c 32962 g 47288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108404
                                                                                                                                                                                                                                                                                                                                                                                                                                  16.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1.08
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Tarvers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 102340
Birren,B., Linton,L.,
Anderson,S., Baldwin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 12, 2000 this sequence version replaced gi:7108213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L6906
Center clone name: 221_C_21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      soon as it is available and the accession number will preserved.
                                                                                                      8866
8966
9990
10090
11333
11433
112598
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13980
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1156 2524: c
2525 2624: gap c
2625 3768: c
5007
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7528
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4907
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                                                                                                                                                                                                                                                                                  3 7627: gap c
                                                                                                                                                                                                                                                                                                                             3 6112: gap o
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4906:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 10
                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 1144 bp in length of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nusbaum, C., Lander, E.,
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of 1415 bp
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of 1006 bp in
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f 1238 bp in
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f 1369 bp in
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* 78446 78545: gap of 100 bp in lei

* 78446 78545: gap of 100 bp

* 78546 81397: contig of 2852 bp in len

* 81398 81497: gap of 2852 bp in len

* 81498 84343: contig of 2846 bp in leng

84444 84443: gap of 100 bp

84444 86480: contig of 2037 bp in lengt

86481 86580: gap of 100 bp

86581 88846: contig of 2037 bp in lengt

88847 88946: gap of 100 bp

88847 88946: gap of 100 bp

88847 88946: gap of 100 bp

88847 88946: gap of 100 bp JUNE 100 bp 10 1 96947 99558 60149 60249 46932 47031; gap of 100 bp 47032 50023; contig of 2992 bp in length 50024 50123; gap of 100 bp 52012 52810; contig of 2687 bp in length 52811 52910; gap of 100 bp 52911 55013; contig of 2103 bp in length 52910 55013; gap of 100 bp 52011 55013; gap of 100 bp 52011 55013; gap of 100 bp 52014 55113; gap of 100 bp 52014 55113; gap of 100 bp 41116 43401: contig of 2286 bp in length
43402 43501: gap of 100 bp
43502 44790: contig of 1289 bp in length
44791 44890: gap of 100 bp
44891 46891: contig of 2041 bp in length 36847 36947 35186 31405 33475 30047 19830 19930 96847 96946: 64849 70718 70618 35086 28812 21214 21313: 014 55113 gap of 100 bp 111 length 57694: contig of 2581 bp in length 195 57794: gap of 100 bp 2595 60148: contig of 2354 bp in length 2354 bp in length 149 60248: gap of 100 bp 100 bp
20811: contig of 1549 bp in 10
12 28911: gap of 100 bp
13 30046: contig of 1135 hn 47
7 30146: gap of 47 30146: gap of 100 bp in 14
47 31304: contig of 1158 bp in 14
05 31404: gap of 100 bp
05 33474: contig of 2070 bp in 14
75 33574: gap of 100 bp
75 33574: gap of 1511 bp in 14
86 35185: gap of 100 bp
86 36846: contig of 1661 bp in 14
47 36946: gap of 100 bp
47 38786: contig of 1840 bp in 14
87 38886: contig of 1840 bp in 14 99657: 93612: 19929: gap of 21213: con 18608: gap of 100 b 19829: contig of 1221 24634: 657: gap of 102370: contig 2470: gap of 27162: 93512: contig of 4566 612: gap of 100 by 96846: contig of 3234 08: gap of 100 bp 24534: contig of 1626 bp 13: gap of 100 by 22808: contig of 1495 contig of 2611 contig of 1284 of. 100 bp 7611 bp in 100 bp f 2713 b 100 bp 100 bp f 2286 bp in length gď dq gd ģ đđ đđ bp in length bp in in in in length length

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REFERENCE
AUTHORS
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                                                                                                                                                                             SOURCE
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                       MEDLINE
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                                                                                                                    AUTHORS
                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                               AP001675 340000 bp DNA
Homo sapiens genomic DNA, Chromosome
AP001675 AL163220 BA000005
AP001675.1 GI:7768691
                                 Nature 405. (6784),
                                             The DNA sequence of human chromosome and sequencing consortium
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                             Homo
                         20289799
           (bases 1 to 340000)
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                                                                                                                                                                           sapiens DNA.
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106208 10911
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1156. .2524
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RP11-221C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11 Human Male BAC"
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137354: gap of 100 bp

143801: contig of 6447 bp 1

143901: gap of 100 bp

143907: gap of 100 bp

148857: contig of 4956 bp 1

148957: gap of 100 bp

156185: contig of 7228 bp 1
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113450; cc
13550
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o: gap of
171697: cc
71797
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109111: ~
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23320: gap of
127732: contig of
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182340: contig of 10543
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118394: contig of
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                                   311-319
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contig of 7189 bp in length
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contig of 8123 bp in
Taylor, T.D.,
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                                   (2000)
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4924 bp
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1412 bp
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4844 bp
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4398 bp
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21q, section 19/105.
 Watanabe, H.,
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The chromosome 21 mapping and sequencing consortium consisting of

* RIKEN Genomic Science Center, Human Genome Research Group, *
Sagamihara 228-8555, Japan,

* e.mail: hattori@gsc.riken.go.jp

* URL: http://hgp.gsc.riken.go.jp/
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info.genome@gbf.de
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* e.mail: nshimizu@dmb-med.keio.ac.
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L163220: Submitted (10-Apr-2000).
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URL: http://www.dmb.med.keio.ac.jp/
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Gattung, S. and Du, Z.
The sequence of C. elegans cosmid T18H9
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Waterston, R.
Direct Submission
Submitted (30-NOV-1995) Robert Waterston
5 (bases 1 to 27710)
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The C. elegans Sequencing Consortium.
Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5' end F07C3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Coding sequences below are predicted from computer analysis, using the program Genefinder(P). Green and L. Hillier, ms in preparation).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University, General USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELT18H9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-JUL-2001) Department of Genetics, Washington University, Genome Sequencing Center, 4444 Forest Park Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waterston, R
Direct Subm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ç
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actual start of this cosmid is at base position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridge CB10 IRQ, England email: rw@nematode.wustl.edu and jes@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanger Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Genetics, Washington University St. Louis , MO 63110, USA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence may not be the entire insert of this clone.
                                                                                                                  /gene="T18H9.2"
/gene="T18H9.2"
/note="similar to the eukaryotic aspartyl proteases
/note="similar to the eukaryotic aspar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSMNUFALHELYRYATLFPKSKKLFDGARIIFWLTVPQIYGVWHLVTYYAVFRESPE
YTEFIRKTLMENLDINVDVVVGPYYYMEDKNGIHDWDWTAFMAMAIWHLIMSSAV
TVFICGYGCYKKITKGLEVSSNSKQTKSIQKQLEYALVVGSAIFFLLMYIPSTVVLFC
TLIQLDVGSASLFISYSIAIYPVVDPLPTLFIYQNYRNAVKSLNDHTDLEYCDKKERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shorter because we only sequence overlapping sections longer because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Hypothetical protein T18H9.4"

/protein 1d="AAA83330.2"

/db_xref="G1:14647338"

/tanslation="MOLTVFNSFLKTAQFVGTCIANPLNIFLIYLILTKSSKKIGNYK

XLMIYVSIYEILFSCSAIVTEPLLHSFTTRVIVIVDVHNSIFSREICSILDCLMCAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1034. .1193,1236. .1552,1602. .1875,
1931. .2097,2141. .2338))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1034. .2338)
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/product="Hypothetical
/protein_id="AAA83331.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="T18H9.2"
join(3031. .304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T18H9.4
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="str-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="T18H9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis
                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="Bristol N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             one m13 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is a gap followed by the cosmid C24B5; 3' cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING COSMID INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       31. .3042,3315. .3680,4857. .4961,5077. .5163,5404,5462. .5590,6436. .6790,6999. .7870,7940.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinxton Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63110, USA,
         1 protein T18H9.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7996)
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gene

/product="Hypothetical protein T18H9.7"
/protein_id="AAK/1873.1"
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FPEVNSIIVTAKLPLSKRNRYLRSNEIKVTPNHGRIDLDCDISFCIQYPHFLKRKSNV

codon_start=1

FNDDASTRSNRRPQLAPFFDSKEKNDHLAAMYEVSDGEGDHGEGGWNSDGDNTKENVA RHRLIQKDSTGSGHPDYSVQTPVRSAGTRVVSSSFDSHSMPHSSTLNSTKNDHGVHRG LQILIQRRKKFKNRLPGGLRDLAVGNINLTYIMQQGGLREIQLNPTSENEVELKGVGA CAGKIFLSSCYSQAPEIVDDRDKQKKNVEDSEDETETDYDDVGDELNEMPSARSGRHK

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```
/note="coded for by the following C. elegans cDNAs: yk5g12.3, yk5g12.5, yk39d6.3, yk39d6.5, yk46b7.3, yk5b57.5, yk79b11.5, yk129h7.3, yk129h7.3, yk129h7.3, yk129h7.3, yk180g2.5, yk180g2.3"
                                                                                                                                                                                          complement(join(17485..17603,17653..18384,18433..18620,
18671..18981,19026..19337,19383..19660,19714..19786,
19834...20058_20107..20191,20441..20529))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTQLLPTSNPKFAQVLPNFNNSSYGSDSASGILGFDTVSFGGISESQLIVPDTVVATABDIDGIMGLGFLANSQQNIYPPFVNAVGQKLVDPIFNYLGHRPNRAGQIFFGGQDTQNCAKYKQYBFLTTGAXYGYWFYPSVSGAYSARANGWTALSDTASSIYYGPKAIVAGIADAAAAAAAAVCYVFYSVSGAYSARANGWTALSDTASSIYTGPKAIVAGIADAAGATNLFLLALVAAALAAVVQVPLVKIEPYRNRLIREGRWVQYRKDREIRRFMMNQSNDMSYGGYYNDYEDEAYVGWITIGFPQQOFKVLIDTGTGSSWAMIPDDITGGTKPENCGSTVPACRGITQFECDDACCGAGAANTDSCFYQNKFDASKSSSYKTMRAFFILEGFGGSARGFLGQDTITFGGGIGEPQLAVPNTYFGQATSLAAFFEGQPLDGILGLAFKSIAVDGSARGFLGQDTITFGGGIGEPQLAVPNTYFGQATSLAAFFEGQPLDGILGLAFKSIAVD
                                                                                                                                                                                                                                                                                                                                                        complement(17485. .20529)
                                                                                                                                                                                                                                                                                                                                                                                                 IVLKYGILEDMIIGGEDEDLYNQEQILHSKRKYYREFTKSAKEIILCSPYTKFTAPTN
FAQCNNYIQSYVNCFSTKCYYCKKHLRQFMPPTVYTRESSPIICHKLCLMSQVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YQLFYKLQEAMDERTVIEKNIIAVSETFRQNAVHAPRVSRLSVPPPLKFSKHVEDANK
GVFLAMDAVMNKTRGDLTWRFKRISHPCFRNSKSLIEVHYCARRPNSEKEFVPCMKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STAGNPAAGRPILTLPSNTTEKHVIALNQWAEVMKSKLEKMRQKSKKALDESMKEHST
MEDLSRAREALSEMGNMYYELNRAAALKCRYNAVFDKRPLYKAVESSIQDLRQKDESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Hypothetical protein T18H9.6"
/protein_id="AAA83333.1"
/db_xref="GI:1118136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(13055. .13151,13216. 14233. .14463,14508. .14588,15197. .:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(13055. .15649)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPYQNQNQIQNQNQYSNYYRTPSLSRGTDSRPVSTATDTDQTKKQSMSTFK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APK I EEREQWWP AY PSLVNP I NPWRYRDENQANALRWRRALGANVDNS I ATQDLMEKL
LPQNAHMRPSDDELLNRQP I AVQASY I DDESDGKLKNEEKQNQQNATQPPYCYTNQNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLQGALRFHRRLQKKQIRPHRFLMLFNLPYSAFFVTAMYLCTKFFYLANVCLQLMFMN
RFLETDKYKWYGMGALVDLLNGTTWEQSGMFPRVSLCDFDVRVMGNMQEHTIQCVLVI
NIFNEKIFILLWFWYLALLVFTFGSFFYWLLVSLWRHLNVRFIIRHLEMSDIAFDSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFGGKPVECLVPDIFSSSWEQYAENYCWASDTYYVPTNEPVAGLQSDEKRQRKISYYQ
WVPFFLLLEAACFRLPSLLWKYLAGHSGIKINEIVKLSSDPNNIKPDIKRANIKSLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Hypothetical protein T18H9.5"
/protein_id="AAA83332.1"
/db_xref="GI:1118135"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to C. elegans unc-7 and drosophila ogre and shaking-B proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(8267.
10307. .10562,10610. .
/gene="T18H9.5"
/note="similar to C. e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(8267. .10741)
/gene="T18H9.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QITPPFINAINQNLVDLPLFTVFLEHEGDQNGVQGGVYTYGGIDTKNCGPVIAYQPLS
SATYYQFKMSAIGSGSYHSSKGWQVISDTGTSLIGGPKAYVSAIADAVGATWRDDYGV
                                                                                                                                                          /gene="T18H9.7"
                                                                                                                                                                                                                                                                                                                    /gene="T18H9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="T18H9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DGAQEKVNRFISNYLKSDGVFVIRMMTLQSGVIFGTDLVQELWRNFHGSEPQLKRSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPFIRQYCNIYDVGTQRVGFAKSLQSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVGSPPQEFRVIMDTGSSNFWIPDSTCDTKATSCHKVLPAPNYSAIPGNFFPKFGPFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="T18H9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YILPCSAKINTLDITIGNOVYNIDSSNTIIPLGDGSNNCIYAIFPFSSGGFGPSWILG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MQSNQQPTTSANASGPSGARISSGNIPHSQSMPVLQSGNTANRP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MVLAAVLSMLRYVGGSDDRDFVDRLHSYFTCNLLIGLAVLVSFK/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:1118134"
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.15649))
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VERSION
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Best Local
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                   This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: RMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquirites: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 15, 2001 this sequence version replaced di:8569972
                                                                                                                                                                                                                                                                                                                                                                                                  During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                       corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gi:13751415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG
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AL357912.10 GI:1
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/protein_id="AAA83334.1"
/protein_id="AAA83334.1"
/db_xref="Gi:11118137"
/translation="MPSIRYRLVALVVFISSVYGOQEAAVVQTPPVQOPTPNLIREGSG
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ITADRIANDOPQICLEDIYDPLRDERPKRNNHAGYIRHPTFQVPQQOVQQFRPAGNVY
IAQDRIANDOSQYFFRADAVVRPYVIPQQQFORQGGSQYIQOQYRPQQQOVSQVFRPAI
IAQDRIANDOSQYFFRADAVVRPYVIPQQFFORQGGSQYIQAYIERPVPARPTFYIERPVP
RDQFVRPVRPVYIAGRLTPGPFIAPVTQGYSERPPATVAPYIERPVPARPTFYIERPVP
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RPVVAPSTTTQRY I EPTTQRPTTRRATTKR I TTTTTAAPTT PRI TTARATTPLATTSR
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26617. .26915,26956. .27037,27086.
/gene="T18H9.1"
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SKKDTAKVTIKAHFKTLLVSRSPSSGSLSLTYLKEKRKDKMLQKLGMKKGQKQKPEEG
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VINRIQNFCHSNSSNPPLTIVGIIGTDKLFSQVVKAYVECLAHKSLANLVNHLRFVAI
PSTSSLFYKMIEGIDPQLDNLCRDLWDRFGDMTLPEKTSLANKIAAWPNSVSSSKMNM
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seauence from
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found at
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Pred. No.
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clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
5.1;
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7,27086. .27411,27487. .27631)
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RESULT :

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SOURCE KEYWORDS

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repeat: matches 3952. .4265 of consensus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is not the entire insert of clone RP11-328N1 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-328N1 is at 1 in this sequence. true left end of clone RP5-1102M4 is at 129958 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/Chrl
RP11-328N1 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
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                                                                                                                                                       /note="L2 repeat: matches 1687. 29487. .29592
                                                                                                                                                                                                                                                                            /note="L1MA3 repeat: matches -1387. .5378 27850. .27996
                                                                                                                                                                                                                                                                                                                   /note="MLT2B repeat: 21183. .27754
  /note="LTR8
33523. .338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1M4 repeat: matches 3258. .3689 of consensus" 1871. .2174
                                        32682.
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29211. .29319
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1. .130057
                                                         'note="AluSx repeat:
                                                                                                                                     /note="L2 repeat: matches 1335.
                                                                                                                                                                                                                                                            note="LlMl/
                                                                                                                                                                                                                                                                                                                                                                            /note="L1MA3 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1MA3 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER20 repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="HAL1 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3365. .8676
/note="11ME1 repeat: matches 5814. .6123 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3814. .8354
/note="LlPA15 repeat:
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/note="L1M4 repeat: matches 3689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1871. .2174
/note="AluSq repeat: matches 1. .306 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171. .1394
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/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluSx repeat: matches 1. .291 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="LIMEc repeat: matches 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MSTC repeat: matches 1. .168 of consensus"
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"LTR8 repeat: matches 1. .691 of consensus" .33812
                                        .33408
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                                                                                                copies 2 mer tt 67% conserved"
                                                                                                                                                                                                                                                       repeat:
                                                                                                                                                                                                                   matches 2064.
                                                                                                                                                                                                                                                         matches 238. .386 of consensus"
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                                                         matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                     matches 427.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          matches 649.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    matches 1. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matches
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                                                                                                                                                                                                                                                                                                                                     .448 of consensus"
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                                                                                                                                     .1441 of
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                                                                                                                                                                                                                              /note="AluYa5 repeat: matches 1.
69724. .69811
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60347. .61105
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                                                     'note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                              note="L1M4 repeat:
                                                                                                                                                                    note="L1MA6 repeat:
                                                                                                                                                                                            70639
                                                                                                                                                                                                            note="MLT1C
                                                                                                                                                                                                                                                                                     'note="MLT1C repeat:
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58960. .69182
                                                                                                                                                                                                                                                                                                                                                                                                note-"L1
                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MER5A repeat: matches 1. .183 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSg repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="59 copies 2 mer ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSx repeat: matches 1. .293 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER44A repeat: matches 57. .330 of consensus"
55356. .55645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="15 copies 2 mer ta 86% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1PA3 repeat: matches 1596. .3569 of consensus"
40964. .43533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36354. .36494
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/note="L1MA7 repeat: matches 5815.
34305. .34552
                                                                                                                                                                                                                                                                                                                           'note="MLTIC repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Alusx repeat: matches 3. .292 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="L1PA13 repeat: matches 5397. .6156 of consensus"
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                                                                                                                                                                                                            .124 of consensus"
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                                                                                                                                                                                                                                                                                                                                                              .5531 of consensus"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Brits, B., Brown, A., Burkett, G., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Campoplano, A., Coastle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, Collymore, Collymore, Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, Dewar, Collymore, Collymore, Collymore, Collymor
Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 20, 2000 this sequence version replaced gi:7342242.
                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,M., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE,
AC027498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome SEQUENCE, 25 unordered p
                                                                                   Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Galagan, J., Gardyna, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 18, clone RP11-656L11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                  Young, G., Zainoun, J., Zimmer, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 180911)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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/note="THE1B-INTERNAL consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88763.
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88763. .89267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="THE1B repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJb repeat: matches 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pieces
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18 clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ginde, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matches 136. .195 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat:
                                                                                                                                                                       and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
4.2;
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RP11-656L11 map 18, WORKING I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .364 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .3102 of consensus'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4548 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .287 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .302 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 1354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,:
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                                                                                                                                                                                                                   Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRAFT
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COMMENT

repeats were identified using RepeatMasker: t, A.F.A. & Green, P. (1996-1997)

in

length

length length

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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y065: contig of 2817 bp in length

9066 9165: gap of 100 bp

9166 13447: contig of 4282 bp in length

13448 13547: gap of 100 bp

13548 17515: contig of 3988 bp in length

17516 17615: gap of 100 bp

17616 21811: contig of 4196 bp in 1-

21812 21911: gap of
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be preserved.
                                                                                                                                                    34676 34775; gap of 100 bp 314776 39152; contig of 4377 bp in lei 39153 39252; gap of 100 bp 39253 44142; contig of 4890 bp in lei 44143 44242; gap of 100 bp 44244 44561; contig of 4319 bp in lei 48562 48661; contig of 5326 bp in lei 48662 53987; contig of 5326 bp in lei 5398 54087; gap of 100 bp 54088 60371; contig of 6284 bp in lei 60372 60471; gap of 100 bp 60472 67910; contig of 67439 bp in lei 67911 68010; gap of 100 bp 68011 74138; contig of 6128 bp in lei 67912 68012; contig of 67904 bp in lei 67913 80242; gap of 100 bp 68014 80242; gap of 100 bp 80143 80242; gap of 100 bp 80143 80242; gap of 100 bp 80143 80260; contig of 7818 bp in lei 68061 88166; gap of 100 bp 80161 88166; gap of 100 bp 95198; gap of 100 bp 95199 95199 95199 95198
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Insert size: 178511; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reassembly program: Phrap; version 0.960731 Consensus quality: 165132 bases at least Q40 Consensus quality: 173168 bases at least Q30 Consensus quality: 176502 bases at least Q20 Consensus quality: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: L845:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2316 2415: gap
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114983: contig of 10246 bp in length
115083: gap of 100 bp
124831: contig of 9748 bp in length
124931: gap of 100 bp
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5: gap of 100 bp
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                                                                                                                                                                          Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C., Melson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F., Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D., Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D., Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, E., Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H., Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V., Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R., Rappuoli, R. and Venter, J.C.
Tettelin,H., Saunders,N.J., Heidelberg,J., Jeffries,A.C., Nelson,K.E., Eisen,J.A., Ketchum,K.A., Hood,D.W., Peden,J.F., Dodson,R.J., Nelson,W.C., Gwinn,M.L., DeBoy,R., Peterson,J.D., Hickey,E.K., Haft,D.H., Salzberg,S.L., White,O., Fleischmann,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis
the complete genome.
AE002395 AE002098
                                                                                                                           Science 287
                                                                                                                                             strain MC58
                                                                                                                                                             Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell death related drug targets in yeast and fungi
Patent: WO 0102550-A 319 11-JAN-2001;
JANSSEN PHARMACEUTICA N.V. (BE)
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                                                                                                                                                                                                                                                                                                                                                                                       Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                           AE002395.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; mitosporic Saccharomycetales; Candida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Candida albicans
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                                                                                                                                                                                                                                                                                                                                                         Neisseria
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE002395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida albicans.
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                                                                                                                                                                                                                                                                                                                                     (bases 1 to 11018)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                         genome sequence of Neisseria meningitidis serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1303 bp DNA
319 from Patent WO0102550.
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/db_xref="taxon:5476"
197 c 196 g 422 t
                                                                                                                                                                                                                                                                                                                                                                                    meningitidis MC58. meningitidis MC58
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                                                                                                                           (5459),
                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:7413428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serogroup B strain MC58 section
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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27;
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 Fleischmann, R.D.,
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-MAR-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medical Center Dr, Rockville, MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGR"
                            GAACGLTVLDCRTQETYRIRARHTVLAGGGLGQIYAATTTPPECTGDAIAMAIRAGCA
                                                     AQGGIAAAWSGEDDIEKHVADTLEAGAGLCDEAAVRAILSQGKPAIEWLLAQGVAFDR
NHNGLHLTREGGHTCRRIAHVADYTGEAVWQSLIAQIRRRPNIRVCERQMALDIQTES
                                                                                                                                             /product="l-aspartate oxidase"
/protein_id="AAF40832.1"
/db_xref="GI:7225614"
                                                                                                                                                                                                                                                                                                similarity; putative"
                                                                                                                                                                                                                                                                                                                               /note-"similar to GB:D13169 PID:42077 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3262. .4770)
/gene="NMB0392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIRQCIGIEDAAAGVAAIKAAGALPIGVGKAEDLGSDIALVSGTAELTYAYLQSVWEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KGVSRDDSLKRILAHGGKTVSEAEFAELTRRKNDNYVEMIQAVKPEDVYPGILPLLEA
LRANGKKIALASASKNGPFLLERMGLTHFFDAIADPAAVAHSKPAPDIFLAAAEGVDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="NMB0391"
2419. .3084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNIGPKGFTGEKYGGATYWDTEAYAVPLYLALAEPEVTRNLLQYRRNQLPQAQHNARE
QGLAGALYPMVTFTGIECHNEWEITFEEIHRNGAIPYAIYNYTNYTGDEGYLAKEGLE
VLVEVSRFWADRVHFSKRNGKYMIHGVTGPNEYENNINNWYTNTLAAWVLDYTREAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVRIDSIIDADVKNEDSNYEEKFWQVLDKGVSDSLSYIAAQTVANPFGVEQFIVNAEQ
TFAGSFKALGGSQTDWQVSNSFESEVGSTPETFEKRVIVTTSRDYQSLEAVKAAGRAL
SEKIAGVAFETLLDAHKAGWLHRWEIADVVIEGSDEAQQGIRFNLFQLFSTYYGEDAR
VGNLEF IQFHPTGLARPSENGRTFLISEAVRGEGGILTNQAGERFMPHYDRRAELAPF
                                                                                                                                                                                                                                                                                                                                                                                           /gene="NMB0392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="beta-phosphoglucomutase"
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/db_xref="G1:7225613"
/translation="MTFTAVLFDLDGVITDTAEYHYRAWKKLAEELGISIDRKFNEQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2419. .3084
/gene="NMB0391"
/note="similar to PID:1495997 percent identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKYPRPDLNVRADELEKWADISANMYRPHDEELGVFVQHDGFLDKDIRPVSALSPDDL
PLNQKWSWDKILRSPFIKQADVLQGIYFFSDRFNIDEKRRNFDFYEPMTVHESSLSPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mytrimeispwilrsaklekehkrlqesltslgngymgmrgsfe
etysadshlgtyiagvwfpdktrvgmwkngyfkyfgkainafnfskykifvdgqevdl
akndvagfsveldwqhgvlrrsftvfgvrfnvckflsvaqkelavirweavsvdgkth
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148. .2406
                                                                                                                   /translation="MQTDCDVLIAGNGLAALTLALSLPESFRIVILCKNRLDDTASRH
                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLDGSHTVALEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWGGKLSFAPFLPSAWTGYAFHINYRGRLIKVAVGKENVVFTLLKGESLDLQVYGKDI
                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="maltose phosphorylase"
/protein_id="AAF40830.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GP:3724125 percent identity:
identified by sequence similarity; putative"
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/strain="MC58"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="GI:7225612"
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                                                                                                                                                                                                                                                                                                                                                                                                                             .4770)
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                                                                                                                                                                                                                                                                                                                                  SP:P10902 GB:X12714 PID:285776 60.55; identified by sequence
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                                                               /product="nicotinate-nucleotide pyrophosphorylase"
/protein_id="AAR40836.1"
/db_xref="GI:7225618"
/translation="MpsekTLFPLPDTLLRPIVEQALSEDLGRRGDITSAAVIAPDKT
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VNHRMGLDDAVLIKDNHLAYCGSIAQAVQQAKQAVGALTCVEIEVDTLAQLDEAIAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="conserved hypothetical protein; identified
Glimmer2; putative"
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/TRANSCENTION-"MQ74ARYVDPLIQDLALETGGCVGDSLEMARGABHEAGTLVVAG
VRFMGESAKILCPEKTVLMPDLEAECSLDLGCPEEAFSAFCDQHPDRTVVYVANTSAA
VKARADWVYTSSVALEIVSYLKSRGEKLIWGEDRHLGDYVGSTSKILKAAVSRPEKKFIVA
NEFKGGELAALKAEHPEAVYLVHPESPQSVIELGDVVGSTSKILKAAVSRPEKKFIVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to SP:P11458 GB:X12713 PID:581137 GB:U00096 PID:1651334 percent identity: 82.02; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                          putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
/protein_d="AAF40835.1"
/db.xref="G1:7225617"
/translation="MDAYPEAEAPPQSIVELVPVLIAVTDGGLRVLTVAQGMLLPNGP
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/gene="NMB0394"
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/gene="NMB0393"
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/gene="NMB0393"
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                      YLTHSSRSLDIGLDFVA"
                                             \mathtt{AERILLDNMDDETLKEAANRCHTQTAHPHTIYCEASGGIGFDRLKRVAQTGVDGIALG}
                                                                                                                                                                                                                                                                                                                                                                                        /gene="NMB0396"
7776. .8657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS ILHPDAKWQDCYGYFPWEDLRTDGGQRDAVVGRLRIWANSADTEEVRQKRLKRIH
LCWGVEPENWSEEYVLQRYEMLYESGLIAEAAEPQANFDFALTGQPMRHDHRRVLATA
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/protein_id="AAF40833.1"
/db_xref="GI:7225615"
/translation="MQMHWLFLTVAILSEVCGSSMLKLSGGFSKLWPSIGVVVSFSVC
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PVQHYTCGGIQTDPCGRTSLPQLYALGETACTGLHGANRLASNSLLECVVTARLCAQA
                                                                                                                                                                                                                                                                                                            /note="similar to PID:665965 SP:P77938 PID:1498753 percent
identity: 67.53; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                              7776. .8657
/gene="NMB0396"
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identified by sequence similarity; putative"
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                                    Submitted (01-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                             Waterston, R.H.
Direct Submission
                                                                                                                                         University MO 63108, U
                                                                                                                                                                                 Submitted (23-FEB-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="transcriptional regulator, ArsR family"
/protein_id="AAF40838.1"
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/protein_id="AAF40837.1"
/db_xref="GI:7225619"
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8685. .8972
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ILFARQRGGIGRAGKRTGGGSFMPSESPPLRLFAKKVGKGTYNPVQSSINI"
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and the Sanger Centre,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality - 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).
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                   TVQQFVNTIYKNKCILKHPIFEQSEPVCGNGVLENGEDCDCGLPGRCSDLNCQPHTCR
FFMHPFFLVLVLASFVAFLVIATWFIVRRYTGTMLNCFKMYKSKHDRGNASPYTNGQI
QILAASPYQNKKMSHSSISGSNTILVSNDSRFATIQRPKVPPPPPPPFRTTIQVVAPGS
                                                                                                                 /translation="mrklsiilvfsciffnvvstleokhieygaavwgakapdyslas
TDSGTTPT IRSLVFVDNKTTAYYEFDMIRVKLMIMKWVDEANOYLNOLGVGLIVVGIIL
QTNRCDLSLOSFHEYEMSRLHKLPDHEFÞATLISYKYAGGLAYVNGMCSSHSUSLSGF
PNEPRAMGSIFFHEVAHLVGVPHRAVNESIYVPNCLCTPKDSLKEDGCLKIPGFDHDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
GQQYETTKVFGSYRESFYDDFSDDEFEEQEVPSAYPLPPGVPTCPAYPPNVPINRVTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(8252. 8406,8464. 8572,9494. 9597,
9653. 9756,9809. 9894,9946. 110146,13178. 13307,
13542. 13628,14243. 14403,14887. 14998,15046. 15146,
15195. 15266,15855. 15995,16043. 16090))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(8252. .16090)
/gene="C34H3.1"
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                                                                                                                                                                                                                                               /protein_id="AAF39762.1"
/db_xref="GI:7206602"
                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                          yk344b12.5; coded for by C. elegans cDNA yk228a1.3; coded for by C. elegans cDNA yk344b12.3"
                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains similarity to Pfam family PF00200 (Disintegrin), score=15.2, E=0.00052, N=1; coded for elegans cDNA yk228a1.5; coded for by C. elegans cDNA
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/chromosome="X"
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/strain="Bristol N2"
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                                                                                                                                                                                                                                                         Submitted (30-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Mar 30, 2001 this sequence version replaced 91:7711703. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                         Estimated Total Number of Errors is 0.1.
Note: Consensus clipped at overlap with AC008790.
Location/Qualifiers
                                                                                                                                                                                                                     www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                 3\, (bases 1 to 34128) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (26-JAN-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                                   www-shgc.stanford.edu
Quality: Phrap Quality >=40 99:8% of Sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 34128)
DOE Joint Genome Institute.
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                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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/protein_id="ABF39763.1"
/db_xref="G1:7206603"
/translation="MLPWQRQVPTSIFPQSNEQVFRMMLAQQHLQLQNFLQQRKMALL
/translation="MLPWQRQVPTSIFPQSNEQVFRMMLAQQHLQLQNFLQQRKMALL
AMNPEIPMITDLKKAKFDFTHMADSIESEQKIKEESVSPKMSPTLTTAAVRPFVPYDQ
PWFMIPGRGRTTGRAARPKKEFICKYCDRHFTKSYNLLIHERTHTDERPYSCDVCGKA
                 /clone="CTD-2170G13"
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/gene="C34H3.2"
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                    Worley, K.C.
Direct Submission
Submitted (07-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 57000)
Direct Submission
                                                                                                                                                                                                                              Unpublished 2 (bases 1
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Submitted (23-MAR-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 23, 2001 this sequence version replaced gi:13173525. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green,

unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < le-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rates than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT-----

Edited+Context	Position Original+Context Edited+Context
0	Number of N's in consensus :
306	Number of consensus changing edits:
0.00374019	Fraction of Phrap values less than 40 :
4.07525e-05	Average error rate (BCM-Phrap estimate):
156142	Phrap values in estimate:
156673	Contig length:
	Summary Statistics

14566 14567 14568	14563	14556	14555	14553 14554	14551	14550	14549	14546	14545	14543	6213	36	Position	
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teceettgte(t)ageatateca cccettgtet(a)geatatecae cccttgteta(g)catatecaet	<pre>tcatcccctt(g)tctagcatat atccccttgt(c)tagcatatcc</pre>	<pre>atgtgaatca(t)ccccttgtct aatcatcccc(t)tgtctagcat</pre>	gatgtgaatc(a)tccccttgtc	<pre>tagatgtgaa(t)catccccttg agatgtgaat(c)atccccttgt</pre>	cctagatgtg(a)atcatcccct	tcctagatgt(g)aatcatcccc	atcctagatg(t)gaatcatccc	tccatcctag(a)tgtgaatcat	ctccatccta(g)atgtgaatca	tgctccatcc(t)agatgtgaat	tctcttgttt(c)tccacgtttt	aaaggtcttt(g)agttttctct	Edited+Context	ts

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tgtctagcat(a)tccactctgt
                                                                                      Indels
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                                                                                      Gaps
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AUTHORS
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gb Qy

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source
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St., Albany, CA 94710, U
5 (bases 1 to 80374)
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Direct Submission
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Submitted (29-APR-1999) P
Street, Albany, CA 94710,
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AC007202
AC007202.3
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Submitted (03-APR-1999) Pl
Street, Albany, CA 94710,
3 (bases 1 to 80374)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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/gene="T8K14.1"
join(448. .3246,
4156. .4303,4397
                                                                                                                                                                         /note="Is a member of the PF(00069 Eukaryotic protei kinase family. ESTs gb[T46484, gb|AF066875 and gb|N come from this gene."
                                                                                                                                                                                                                                                        join(448. .3246,3320. .3391,3652.
4156. .4303,4397. .4519,4737. .48
/gene="T8K14.1"
                                                                                                                                                                                                                                                                                                                                                   448. .5132
                                                                                                                                                                                                                                                                                                                                                                     /chromosome="1"
/clone="T8K14"
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                  652. .3804,3894.
.4824,4933. .51
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FAPDANSKIVPATAIPDGWMGLDIGPDSIKTFSEALDTTKTIIWNGPMGVFEFDKFAA
GTEAVAKQLAELSGKGVTTIIGGGDSVAAVEKVGLADKMSHISTGGGASLELLEGKPL
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/db_xref="G1:4835754"
/tanslation="MATKRSVGTLKEADLKGKSVFVRVDLNVPLDDNSNITDDTRIRA
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AVPTIKYLMGNGSRVVLLENVRFYAEEEKNDPEFAKKLAALADVYVNDAFGTAHRAHAST
VQKLVAGLPEGGVLLLENVRFYAEEEKNDPEFAKKLAALADVYVNDAFGTAHRAHAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Is a member of the PF|00162 Phosphoglycerate kinase family. ESTS gblN38721, gb|T22178, gb|R90345, gb|R90715, gb|R913140, gb|R46295, gb|H37082, gb|R46076, gb|R37132, gb|AA597649, gb|AAI100648 and gb|Z48462 come from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QQKCEQSVSYEKKRLLAVHEAGHIVLAHLFPREDWHAFSQLLPGGKETAVSVFYPRED.
MVDQGYTTFGYMKMQMVVAHGGRCAERVVFGDNVTDGGKDDLEKITKIAREMVISPQS
ARLGLTQLVKKIGMVDLPDNPDGELIKYRWDHPHVMPAEMSVEVSELFTRELTRYIEE
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GFPLEYIVDIPLDPYLFETICNAGVEVDLLQKRQIHYFMKVFIALLPGILILWFIRES
AMLLLITSKRFLYKKYNQLFDMAYAENFILPVGDVSETKSMYKEVVLGGDVWDLLDEL
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/protein_id="AAD30220.1"
/db_xref="Gi:4835753"
/translation="MEIAISYKPNPLISSSTQLLKRSKSFGLVRFPAKYGLGATRKKQ
LFRYYASESSSGSSSNSDGGFSWVRLAQSIRLGAERIGEKIGESYKTEIGFDSEEASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(5680. .5757,5848. .5928,6021. .6128,
6221. .6295,6397. .6516,6700. .6876,6987. .7103,7197. .7316,
7406. .7443,7567. .7787,7887. .7999,8095. .8262,8367. .8507,
8611. .8853,8933. .9010,9243. .9520,9737. .9963,10170. .10354,
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SEEFGAMVENLRTPDSEPKDEKTETRHAALPPLGSEFFDYSGLQIIKNEDLEELRELGS
GEFGTVYHGKRRGSDVAIKRIKKSLFAGRSSEDGERLTGEFWGEAEILSKLHPNVVAF
GTVKNGGPGGTLATVTEYMVDGSLRVLVKNDHLDRRKRLIIAMDAAFGMEYLHSKN
TVHFDLKCDNILLVNLKDPSRPICKVGDFGLSKIKRNTLVSGGVRGTLFWMAPELLNGS
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TVRPYPHDGAAVSMNVQNHDRKNWSYFQQLAEDQFIQRDVVLDQADSRIPSDRKDGGE
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GKSHDEFKTVNDDANHHTHKDVETIFEKVGVSDETLESEPLHKIVNPDDANKNRVVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TEELAMNALRANRHILDLITRELLEKSRITGLEVEEKMKDLSPLMFEDFVKPFQINPD
DEELLPHKDRVSYQPVDLRAAPLHRS"
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KNLAEDIDFGKANIRNLVNEAAIMSVRKGRSYIYQQDIVDVLDKQLLEGMGVLLTEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(5680. .11012)
/gene="T8K14.2"
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LPPSRDPRQNTTAKPATYRDAVITGQVPLSGIEDQLSTSSSTYAPVHSDSESNLIDLN
                                                                                                                                                             EGVAKFLKPSVAGFLMQKELDYLVGAVANPKKPFAAIVGGSKVSTKIGVIESLLNTVD
ILLLGGGMIFTFYKAQGLSVGSSLVEEDKLDLAKSLMEKAKAKGVSLLLPTDVVIADK
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KSGAAKINEMFSIARRNAPAFVFVDEIDAIAGRHARKDPRRRATFEALIAQLDGEKEK
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LGYSGEIGDSYGNWRERLATWKEMLEREKLSEQLNSSAAKYYVEFDMKEYEKSLREDY
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LMEECWAPNPMARPSFTEIAGRLRVMSSAATSTQSKPSAHRASK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="T8K14.3"
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18; Conserv
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19928. .20028,20168. .20280,20369. .20468,20547. .20693,
20774. .20834,20925. .21022,21110. .21252,21361. .21444,
21529. .21618,21702. .21756)
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/gene="T8K14.4"
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/protein_id="AAD30223.1"
/protein_id="AAD30223.1"
/protein_id="AAD30223.1"
/db_xref==01:4835756"
/translation="MAFSSLLRSAASYTVAAPRPDFFSSPASDHSKVLSSLGFSRIGRLVLFSRFSGSISSLQNGBARSVOPIKATATEVBAYVRFSSSSGKKWGINGFGRIGRLVLFRFSRFDIEVVAVNDPFIDAKYMAYMLKYDSTHGNFKGSINVIDDSTLEINGKKUVLFRIATSRDDIEVVAVNDPFIDAKYMAYMLKYDSTHGNFKGSINVIDDSTEINGKKUVLVRIATSRDDIEVVAVNDFTDAKYMYMLKYDSTHGNFKGTISAPSADAPMFVVGVRHTYQPNMDIVSNASCTTNCIAPLAKVVHEEFGILGGLMTVHATTATQKTVDGPSMCHWFGGFASQNIIFUSNASCTTNCIAPLAKVGVLPELNGKLTGMAFFVPTSNUSVDLTCRLEKGASYEDVKAAIKHASEGPLKGILGYTDEDVSNDFVGDSRSSIFDANAGIGLSKSFV
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                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
/protein_id="AAD30224.1"
/db_xref="GI:4835757"
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KKILVTPPSCVKLIHGLCKREQLDAAIEVFLYTLDNNFKLMPRVCNYLLSSLLESTEK
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/translation="""
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AP003046
                                                                                                Direct Submission
Submitted (13-DEC-2000) Takuji Sasaki, National Institute of
Aarohiological Resources, Rice Genome Research Program; Kann
           Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Mar 28, 2001 this sequence version replaced gi:11862976.
Genes were predicted from the integrated results of the following:
                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 GENSCAN1.0,
                                                                                                                                                                                                                                 clone: P0445D12
                                                                                                                                                                                                                                               Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                             Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (cultivar:Nipponbare) DNA, clone:P0445D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Sep 9, 2000 this sequence version replaced gi:9256045. Draft Sequence Produced by DOE Joint Genome Institute
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                                                                                                                                                                      Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                          Published Only in DataBase (2000) In press
                                                                                                                                                                                                                                                                   Sasaki,T., Matsumoto,T.
                                                                                                                                                                                                                                                                                                                                                                                                                      AP003046.2 GI:13486797
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Mammalia; Eutheria; Pr
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The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0445D12 clone has an overlap with P0684C01 (DDBJ: AP002487) clone at the position I to 17,951 of 5' end. The sequence of this clone starts at the position 60650 of P0684C01. Detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A gene with identity or significant homology to a protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     corresponding DDBJ accession no. and RGP clone ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the identified cDNA sequences using BLASTN 2.0 with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI NonRedundant Protein database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (October 1998 version).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein homologies of the coding regions were searched against NonRedundant Protein database with BLASTP2.0. ESTs represent
RDGPTNKVRARMSVASAIIFGSVFWRMGKTQTSIQDRMGLLQVTAINTAMAALTKTVG
VFPKERAIVDRERAKGSYALGPYLSSKLLAEIPIGAAFPLIFGSILYPMSKLHPTFSR
FAKFCGIVTVESFAASAMGLTVGAMAPTTEAAMALGPSLMTVFIVFGGYYVNPDNTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(join(17738..17923,18232..18316,18417
18768..18988,19165..19296,19872..20148,20541.
21433..21565,21895..22045,22138..22328,22821.
/gene="P0445D12.3"
complement(join(17738..17923,18232..18316,18417
                                                                                                                                                                   ELQLRRTLTPERKESYVNDLLFRLGLVNCADSIVGDAKVRGISGGEKKRLSLACELIA
SPSIIFADEPTTGLDAFQAEKVMETLRQLAEDGHTVICSIHQPRGSVYGKFDDIVLLS
                                                                                                                                                                                                                                                               /translation="mevrglgQtLaALaAaLfvravAgPgFALLPPADDEDSDADPEA
GGEGGGVPPVTIRWARITCALKNKRGDVARFLLSNASGEAKSGRLLALMGPSGSGKTT
                                                                                                                                                                                                                                                                                                                             /product="putative ABC transporter"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MSSSMSLLTSPAELGRRGPALKARRSSPAACCAFRRDQYSGGAL
VDSSMAVLRRRMREARMAENNYEAPAGWSAWEKRYYPAYVSDVSAAVGALQLLLMGTR
PSVAIAAAALLFAGYPVSAVAAVHHLAQLAAESAVLLQHHVVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB40030,1"
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ATTRSILAWFCLADSYQTTCLQKLKQALNPNKAMSPKCTVRSSPLIIHSARQLKDRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(3938. .4150,5347.
/gene="P0445D12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(3938. .4150,5347. /gene="P0445D12.1"
                                                                                                  EGEVIYMGPAKEEPLLYFASLGYHCPDHVNPAEFLADLISVDYSSAESVQSSRKRIEN
LIEEFSNKVAITESNSSLTNPEGSEFSPKLIQKSTTKHRRGWWRQFRLLFKRAWMQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18768. .18988,19165. .19296,19872. .20148,20541.
21433. .21565,21895. .22045,22138. .22328,22821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(16002..16439)
/gene="P0445D12.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0445D12.2"
comp]emert(177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKLTWSESKQSRSAIIIR"
                                                                                                                                                                                                                                    LLNVLAGQLTASPSLHLSGFLYINGRPISEGGYKIAYVRQEDLFFSQLTVRETLSLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="BAB40031.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains ESTs AU093168(C0321),D15235(C0321)
                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0445D12.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:13486799"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="P0445D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .140952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5445,6717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5445,6717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .18316,18417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .18316,18417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .6767))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .20742,
.23036))
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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
/translation="marlamTyrramogograygdTmahssrsgdogreggyaagTacgd
RAARCGRPARDAGAHSCRSGGRCDGGATTGYATRRROPATPHRYASDAMAPSCRSDGP
                                                                                                                                                                                       complement(join(44730. .44939,45033.
                                                                                                                                                                                                                                                                 VSPSPCGVGVGAAVCVACVRANGDDAAAAQYKCKLWVEVPTNSDNMVMMTSKVRSSDL
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ESAKRGPLVVATAMIDDPQIDVRIAVGLLHCHACLLPLKPPVFKCEAAHVVCSGCRGNH
GQLCRRAAAYAHCAELDAIVGAAKVACAHAPYGCDSYVYYGAAAEHQRACPCAPCSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NGAGDSKLGGGARREERDGEGEQENEKEGELGSASAHAHARATHGRDEGEEG'
join(42735. .42995,43154. .43891)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MGRPAREGGPRHAREGRRGGASGPGSPRVVPSGTRLSVARFTVR
REHAARAR INGRDAVHARGSRCCGCGGTRSLMAHGGPRARAGGRGAADRGRLDPVLA
ELAPTWRLKGCHTGRREVEDDAGQNGRRTAAYNGGANHGDTGGSGHTWHLETPRODD
TARIRRELDGGGLRRRQPSAREGGNGDGATGGRFGRARASTRLRESVSSVRLDGDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(38187. .38413,38479. .38682,39059./gene="P0445D12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(38187. .38413,38479. .38682,39059./gene="P0445D12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRFRSSPAALPGHLAAGHSWPVAEIAYGKPKKLAVPPPAHVLVGEADRAVFLVSSCAV
GAGAAVCVVCVRANGGGDNAAAVARYKCKLWVEVPSNDDNMAMMTSMVRSSDLAGGFP
AADKGMLLWVPPEMLHGVPGGEAAILSIRIDRAAAATPKFTTTRARSQKGMH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VTMAAMEQTEEETQIDVRIAVALLHCHACLQPLKPPVFKCDEAHIVCSGCRCGHHGQL
CGGAAVYSHCAELDAIVATAKVPCAHAPYGCSSYVVYAGVADHQRACPCAPCSCPEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAB40034.1"
/db_xref="GI:13486802"
/translation="MVEQNKRARANGEVKQEQQQEEEEEVEEGEVSQEETQRTGAFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSDFRNSTVNSDMRYMEWDDPPQMEPHFLNTTHYDEIVESGVPFARKFRENEPLLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSRAAPAVRAFGNVDVVGRPTAGTPMGSSGLAATLRAAAALLRLDSEWDWFVTLNAAD
YPLVTQDDLIHVFSSVPRHLNFIDHTSDIGWKETQRVQPIIVDAGIYLAGRNQFFQAT
EKRDTPDGFKFFTGSPWVILNRRFIEYCIFGWENLPRTLLMYFTNVMLPQEGYFHSVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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/db_xref="G1:13486801"
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/translation="MGAADKWLLPLVSVSFVSLLLFLSALSGFSASSSLFARLPPPSY
VRRGAAAPPSFAYVLSGGRGEGRKLLFLLLAVYHPRNRYLLHLSADAPESERVELAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFRWIPKVSLIRWAFQGLCINEFKGLQFEQQHSYDIQTGEQALERFSLGGIRIADTLV AQGRILMFWYWLTYLLLKKNRPKYQQLLPPSEEDQNKQQVKEVK" join(25341. .25842,28143. .28218,28300. .28415,28495. .2900
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/db_xref="GI:13486805"
                                                                                                                                                                                                                                      complement(join(44730. .44939,45033.
                                                                                                                                                                                                                                                                                                                     DPGCGFRGSPAALLGHFATDHPWSVTQISYAKPCRLAVPLPRRCHVLVGEDDRAMFLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(42735. .42995,43154. .43891)
/gene="P0445D12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt RRLASCHFGKRRKEREGDEAVGGGALPPILGSMRGGRQALTAAATGRSATTARARAGS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="BAB40035.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jυτη(33714. .33962,34268.
/gene="P0445D12.5"
inin/227".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(25341. .25842,28143.
/gene="P0445D12.4"
                                                                                                                                                                                                                /gene="P0445D12.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0445D12.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt REAGDVWALPSTGGDGGEHTASGGNGRSKSKLALGGHGQNGDREDDAGGEKKEERKGE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(33714. .33962,34268. .35005)
/gene="P0445D12.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="P0445D12
join(25341. .25
                                                                                                                                   'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDERVLHRWRHRPVPGAWCTGRKRWFNDPCSQWSNVNIVRPGPQAEKFRKHMNQIIEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains ESTs AU161457(C63275),AU161458(C63275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .25842,28143.
5D12.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .28218,28300. .28415,28495. .29009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .35005)
                                                                                                                                                                                       .45272))
                                                                                                                                                                                                                                        .45272))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 22
AL161454/c
                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                            requests: clonerequest@sanger.ac.uk
on Jun 14, 2001 this sequence version replaced gi:14269905.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="3' LTR"
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/gene="p0445D12.10"
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EEEEEEVQAGGMIAAAVGDGFEGVEISVRIDLAVLHCPLCLLPLKPPTYQCAAGHLACS
SCHGDVPGKKCHTCGGGGGGGVYARCPGLDTFLRAAKILCPNDLFGCRSYVAYHDVAA
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/db_xref="GI:13486807"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapp
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RP11-72B4 is from the library RPCI-11.1 constructed
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VECTOR: pBACe3.6
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                                                            note="L1ME2 repeat: matches 5913. .6162 of consensus"
                                                                                                    note="MER5A repeat:
                                                                                                                                             'note-"THE1C
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/db_xref="taxon:9606"
/chromosome="9"
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                                                                                                                                                                note="L1PA3 repeat: matches 5359. .6142 of consensus"
4647. .15016
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e="THE1B repeat: matches 1...364 of
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.e="L1MC4 repeat: matches 7813. .7952 of consensus"
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1. .10623
                                                                                                                                                                                                                                                                     -"MLTID repeat:
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                                     50430.
                                   /note="L1MC2 repeat: matches 5193. .6224 of consensus"
i0430. .50717
                                                                                                                                               /note="AluSg :
39570. .40190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   restriction
                                                                                                                                                                                                                                                                                                                                                  note="L1MD1 repeat: matches 5374. .6224 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                        note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                          note="L1MEc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1MD repeat: matches 179.
32004. .32557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluY repeat: matches 1. .296 of consensus"
18257. .18527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Single clone region. Assembly confirmed
restriction digest data."
                                                                                                                                                                                                                                                                            'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                'note="MIR repeat: matches 177. .256 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="MER11C repeat: matches 1. .1071 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluSc repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1 repeat: matches 3596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Alusx repeat: matches 64.
                                                                                                                                                                                                                                        note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="L1M4c repeat: matches 1489. .1687 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1MB3 repeat: matches 5893. .6175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .e="L1MD repeat: matches 21. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="L1M4 repeat: matches 2773. .2896 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e="TIGGER1 repeat: matches 1. .1792 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="L1M4 repeat:
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                                                              .45707
                 "AluSc repeat: matches 1.
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.21472
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                                                                                                           .40792
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                                                                                                                            414.
                                                                                        883.
                  . 287
                                                                                                                                                                                                                                                                            .304 of
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AL359815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agatgccttacaaccctg 35
                                                                                                                                                 Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET-amersham; 6% of reads Dye-terminator Big Dye; 93% of reads Consensus quality: 143907 bases at least Q40 Consensus quality: 144683 bases at least Q30 Consensus quality: 144683 bases at least Q20 Consensus quality: 145097 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 4, 2001 this sequence version replaced gi:14587003.
                                                                                             Insert size: 145671; sum-of-contigs
Insert size: 155726; 1.2% error; agarose-fp
Quality coverage: 7.35x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                           Center project name: bA63N8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 146571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome
                                                                               coverage: 7.63x in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                           Center code:
                                                                                                                                                                                                                                                                                                                                                                                                         Center: Sanger Centre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ***, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSg repeat: 54520. .54819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MER3 58211. .5860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57861.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="L1MC4 repeat: 56527. .56852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="TIGGER2 repeat: matches 1461. .2718 of consensus" 52344. .52629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="L1MC4 repeat:
58890. .59017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L1MB6 repeat: matches 5258. .6004 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSc repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MB6 repeat: matches 4937. .5258 of consensus" 56853. .57142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="AluSx repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146571 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%;
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Pred. No.
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1 clone RP11-63N8,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 matches 1.
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15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7699. .7827 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .291 of consensus"
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SEQUENCING IN
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24805 24904: gap of
24905 35138: contig of 10234 bp in length
35139 35238: gap of
35139 35238: gap of
35139 54888: contig of 19650 bp in length
54889 54988: gap of
54989 69175: contig of 14187 bp in length
69176 69275: gap of
69276 84233: contig of 14958 bp in length
69276 84233: contig of 14958 bp in length
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84234 84333: gap o
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102447 116814: contig of 14368 bp in length
116815 116914: gap of 100 bp
116915 122988: contig of 6074 bp in length
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                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment:02746
fragment_chain:2"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="assembly_fragment:01308
fragment_chain:2"
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                                                                                                                                                                        /note="assembly
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fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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/db_xref="taxon:9606"
/chromosome="1"
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146571: contig of 23483
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AC034225
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                                                        source
                                                                                                                                                                                                     * by the finished sequence as soon as it is available and the accession number will be preserved.

* the accession number will be preserved.

* 61863 61962: contig of 61862 bp in length 61963 68022: contig of 6060 bp in length 68023 80136: contig of 12014 bp in length 80137 80236: gap of unknown length 80137 80236: gap of unknown length 80237 80311: contig of 3075 bp in length 80237 83311: gap of unknown length 83412 88833: contig of 5422 bp in length 83412 88833: gap of unknown length 92360: contig of 5422 bp in length 92360: contig of 5427 bp in length 92360: contig of 3427 bp in length 92360: contig of 3427 bp in length 92360: contig of 3427 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Consensus quality: 139048 bases at least Q40
Consensus quality: 147965 bases at least Q30
Consensus quality: 147145 bases at least Q20
Estimated insert size: 150000; pulse field gel estimation
Estimated insert size: 148148; sum-of-contigs estimation
Quality coverage: 5.82 in Q20 bases; pulse field gel estimation
Quality coverage: 5.89 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Joint Genome Institute
Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 148498)
DOE Joint Genome Institute.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC034225.4 GI:9256727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing of Human Chromosome
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Joint Genome Institute.
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88934
92361
92461
120403
                                                                                                             120503
/db_xref="taxon:9606"
                      /organism="Homo sapiens"
                                                                              Location/Qualifiers
                                                                                                        92460: gap of unknown length
120402: contig of 27942 bp in
120502: gap of unknown length
148498: contig of 27996 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid: LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 150971 bases at least Q40 Consensus quality: 151464 bases at least Q30 Consensus quality: 151889 bases at least Q20
                                                                                                                                                                                                                                                                                                                       * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 152505; sum-of-contigs
Insert size: 157709; 4.7% error; agarose-fp
Quality coverage: 7.00x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: bA35C9
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-MAY-2001) Sanger Centre, Hinxton, Cambridgesh: CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coverage: 6.89x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burton,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
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                                     54731 54830: gap of 100 bp
54831 75701: contig of 20871 bp in length
75702 75801: gap of 100 bp
75802 85440: contig of 9639 bp in length
                                                                                                                                                   51406 51505:
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21952 3698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk
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116412: cont
                                                                                                                                                                    551: gap of 100 bp
36986: contig of 15035 bp in length
366: gap of 100 bp
51405: contig of 14319 bp in length
                                                                                                                               54730:
                                                                                                                                                                                                                                                        21851: contig of 21851 bp in length
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  of 30872 bp in length
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116413 116512:

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                                                                                                                                                                                                                                                           AATTTATTCCACACAACA 37948
                                                                                                                  Homo sapiens chromosome 4 clone RP11-394N5 map 4, WORKING DRAFT SEQUENCE, 28 unordered pieces. AC023537.2 GI:7229813
               Birren, B., Linton, L., Nusbaum, C.
                                                                                                         HTG;
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                   Similarity
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                             (bases 1 to 156795)
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141141 145417
sapiens chromosome 4, clone RP11-394N5
                                                                                                     HTGS_PHASE1;
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145518 153405: contig of 7888 bp in length
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85541. .1
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fragment_chain:2"
145518. .153405
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fragment_chain:2"
    40678 c    42451 g    36301 t
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141141. .145417
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/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:02336
fragment_chain:2"
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fragment_chain:2"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP11-35C9"
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                                                                                                     HTGS_DRAFT
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0: contig of 24528 bp in length
gap of 100 bp
7: contig of 4277 bp in length
100 bp
100 bp
100 bp
110 ap 150 length
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                                                                                                                                                                                                                                                                                                                   0;
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              and Lander, E
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Morman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Mux., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-FEB-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 12, 2000 this sequence version replaced gi:6978216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DeArellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M., Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                     Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 137441 bases at least Q40
Consensus quality: 147789 bases at least Q30
Consensus quality: 151521 bases at least Q20
Insert size: 154000; agarose-fp
Insert size: 154005; sum-of-contigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 3.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 394_N_5
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5543
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COMMENT

as soon as it be preserved. 5097 5196: gap of 100 bb 5197 5196: gap of 100 bb 5197 7059: contig of 1863 bp in 1 7060 7159: gap of 100 bp 7160 9463: contig of 2304 bp in 1¢ 9464 9563: gap of 100 bp 11761 11860: gap of 2014 bp in 1¢ 11761 11860: gap of 100 bp 11861 13457: contig of 1597 bp in len 13458 13557: gap of 100 bp 13558 15559: contig of 7000 soon as it is available and the accession number will 2957: contig of 1446 bp 2958 3057: gap of 100 bp 3058 5096: contin 100 bp 1411: contig of 1411 bp in length 1: gap of 100 bp 2957: contig of 1446 bp in length bp in length bp in length Length length length length

5560 15659:

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FEATURES
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81246 88655
88656 88755 97086
97087 97186: 93
97187 107056: 53
107057 119495
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28 24224: contig of 2097 bp
25 24324: gap of 100 bp
25 26969: contig of 2645 bp
70 27069: gap of 100 bp
70 30436: contig of 3367 bp
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Location/Qualifiers
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    /note="assembly_fragment"
24325. .26969
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11861. .13457
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/db_xref="taxon:9606"
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88655: contig of 7410 bp in 16
6 88755: gap of 100 bp
97086: contig of 8331 bp in let
97186: gap of 100 bp
106956: contig of 9770 bp in 107056: gap of 1070 bp in 107056: gap of 1
                                                                                                                   'note="assembly_fragment"
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/clone_lib="RPCI-11 Human Male
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22027: contig of 1805
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20122: contig of 1687
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REFERENCE
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SOURCE
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AC024315/c
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collymore, A., Cooke, P., Choepel, Y., Grant, G., Didaz, J.S., Dodge, S., Domino, M., Doyle, M., Fernestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                              1 (bases 1 to 165858)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-26N3
Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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134467. .156795
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88756. 97086
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119596. .134366
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97187. .106956
/note="assembly_fragment"
107057. .119495
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81246. .88655
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27070. .30436
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72969. .81145
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44187. .49895
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100.0%;
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SEQUENCE, 14 unorc
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Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lileu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Piarre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wolx, M., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Romay 25, 2000 this sequence version replaced gi:7239607. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howland, J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
                           27436 41698: contig of 14263 bp in length
41699 41798: gap of 100 bp
41799 54767: contig of 12969 bp in length
54768 54867: gap of 100 bp
54868 70875: contig of 16008 bp in length
70876 70975: gap of 100 bp
70976 87982: contig of 17007 bp in length
87983 88082: gap of 100 bp
87983 88082: gap of 100 bp
110114 110213: gap of 100 bp
110114 110213: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number
                                          88083
110114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 4.6 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 0.960731 Consensus quality: 154942 bases at least 040 Consensus quality: 159890 bases at least 030 Consensus quality: 162505 bases at least 030 Consensus quality: 162505 bases at least 020 Insert size: 164558; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L4668
Center clone name: 26_N_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                             100 bp

18/54 27335: contig of 8582 b

27336 27435: gap of 100 bp

11699 41700
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1275 1374: gap of 100 bp
1375 2528: contig of 1154 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                    6547: gap of 100 bp
11790: contig of 5243
11890: gap of 100 bp
18653: contig of 6763
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28: gap of

4506: cor
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contig of 23547 h
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contig of 1841 bp in length
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contig of 1878 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, AC009776
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 12 clone RP11-333I15, WORKING DRAFT SEQUENCE, 22 unordered pieces.
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Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,
Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C.,
Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F.,
Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R.,
                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I (bases 1 to 183496)

1 (bases 1 to 183496)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Banks,T., Falsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Falsbrooks,S.L., Amaratunge,H.C., Banks,T., Falsbrooks,S.L., Amaratunge,H.C., Banks,T., Falsbrooks,S.L., Amaratunge,H.C., Banks,T., Falsbrooks,S.L., Banks,T., Bank
                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                 Eukaryota;
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                             Metazoa;
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Foster, P., Frantz, P., Gabisi, Ferrayun, Forter, Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Harr, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Moser, M., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nwokenkwo, S., Oyuh, M., Okwuonu, G., Oragunye, N., Pace, A., Pace, A., Payton, B., Peery, J., Peters, L., Pickens, R., Primus, E., Pu, L.L., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Tamerisa, K., Tang, H., Shooshtari, N., Stone, H., Shooshtari, N., Watliams, S., Watle, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Wang, S., Watliams, G., Williamson, A., Washington, C., and Gibhs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on Oct 2, 2000 this sequence version replaced gi:10047636.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 22 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
                                                                                                                                       as soon as it is available and the be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chemistry: Dye-primer Bodipy: 61% of reads chemistry: Dye-terminator Big Dye: 39% of reads Assembly program: Phrap; version 0.990329 consensus quality: 165672 bases at least Q40 consensus quality: 174319 bases at least Q30 consensus quality: 174319 bases at least Q30 consensus quality: 17820 bases at least Q20 Estimated insert size: 176791; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: HMJH
Center clone name: RP11-333115
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 3.8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.hgsc.bcm.tmc.edu/
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29141
29040: contig of 29040 bp in length 29140: gap of unknown length 48361: contig of 19221 bp in length
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

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COMMENT

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                       AC068581
                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
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Best Local :
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 19063)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                        18;
                                        Homo sapiens
                                                           AC068581.2 GI:10280770
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                SEQUENCE, AC068581
                                                                                                  AC068581 190663 bp DNA HTG 23-SEP-2000 HOMO sapiens chromosome 4 clone RP11-598012 map 4, WORKING DRAFT
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                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
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39432 c 39724 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 23, 2000 this sequence version replaced gi:7705127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Tailamas,J. Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J. Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Yeyung,G., Zainoun,J., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Campopiano, A., Castle, A., Choepel, Y., Colango
Collymore, A., Cooke, P., DeArellano, K., Dewar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N. Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.
Campopiano,A., Castle,A., Cheepel,Y., Colangelo,M., (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  as soon as it is available and the accession number will be preserved.
                 4554 4653; contig of 4553 bp in length
4554 4653; gap of 100 bp
4654 5713; contig of 1060 bp in length
5714 5813; gap of 100 bp
5814 9313; contig of 3500 bp in length
9314 9413; gap of 100 bp
9414 12245; contig of 2832 bp in length
12246 12345; gap of 100 bp
12346 15186; contig of 2841 bp in length
15187 15186; contig of 3876 bp in length
15187 15162; contig of 3876 bp in length
19163 19262; gap of 100 bp
19163 23897; contig of 4635 bp in length
19163 23897; contig of 4635 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: M13; M77815; 100% of reads Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 177622 bases at least Q30 Consensus quality: 184698 bases at least Q30 Consensus quality: 186982 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
----- project Information
Center project name: L10318
Center clone name: 598_O_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeats were identified using RepeatMasker:
L, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.0 in Q20 bases; agarose-fp Quality coverage: 4.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert size: 194000; agarose-fp
Insert size: 188563; sum-of-contigs
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Grant,G., Hagos,B., Heaford,A., Horton,L.,
Grant,G., Johnson,R., Jones,C., Kann,L., Kara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Research
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154910
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27486 27585: gap of 100 bp
27586 31745: contig of 4160 bp in length
31746 31845: gap of 100 bp
31846 36461: contig of 4616 bp in length
                                                                                                                                                               /note="assembly_fragment"
67876. .77789
                                                                                                /note="assembly_fragment"
77890. .86920
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59053. .67775
                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
50764. .58952
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/db_xref="taxon:9606"
/chromosome="4"
/note="assembly_fragment
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19263. .23897
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/clone_lib="RPCI-11 Human
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Location/Qualifiers
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;; gap of
125542; cc
15642
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141160: contig of 15518 l
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110977: contig of 23957 bp
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TITLE
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                             Consensus quality: 177736 bases at least Q40
Consensus quality: 184740 bases at least Q30
Consensus quality: 186701 bases at least Q30
Consensus quality: 186701 bases at least Q30
Estimated insert size: 192000; agarose-fp estimation
Estimated insert size: 192000; agarose-fp estimation
Quality coverage: 8.68 in Q20 bases; agarose-fp estimation
Quality coverage: 8.74 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 18 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                              ------Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joi Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity 100
18; Conservative
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DOE Joint Genome Institute.
Sequencing of Mouse
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Mus musculus clone
                                                                                                                                                                                                                                                                                                 Summary Statistics
                                                                                                                                                                                                                                                                                                                               Center clone name: RPCI-23_373B15
                                                                                                                                                                                                                                                                                                                                               Project Information
Center Project Name: 1880143
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                  Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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154918. .176781
/note="assembly_fragment"
176882. .190663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_fragment"
141261. .154817
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125643. .141160
                                                                                                                                                                                                                                                                                                                                                                                              http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.6%; Score 18; DB
100.0%; Pred. No. 15
live 0; Mismatches
1123: contig of 1123
1223: gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .125542
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15;
   bp in length
length
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AL357568
                                  COMMENT
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Best Local :
                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                             PROGRESS
AL357568
                             Submitted (03-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 7, 2001 this sequence version replaced gi:12329367.
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
                                                                                                     Direct Submission
                                                                                                                      Burton, J
                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                        AL357568.11 GI:13990061
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                         Homo sapiens chromosome 1 clone RP11-506024, PROGRESS ***, 8 unordered pieces.
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/db_xref="taxon:10090"
/clone="RP23-373B15"
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                 Genome Center
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Pred. No.
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g of 20973 bp in
f unknown length
g of 25817 bp in
f unknown length
g of 19556 bp in
f unknown length
g of 27388 bp in
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g of 9610 bp in le
f unknown length
g of 12325 bp in
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of 8497
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of 6136
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of 3431
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of 2360
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of 1739
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DB 2; 15;

Length 192430;

23" others

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Indels

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SEQUENCING IN 03-MAY-2001

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert size: 197905; sum-of-contigs
Insert size: 138913; 37.8% error; agarose-fp
Quality coverage: 7.56x in Q20 bases; sum-of-contigs Quality
coverage: 10.97x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:
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25146 25145: gap of 100 bp
25146 33473: contig of 8328 bp in length
33474 33573: gap of 100 bp
33574 79364: contig of 45791 bp in length
79365 79464: gap of 100 bp
79465 114464: contig of 24600 bp in length
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                                                                                                /note="assembly_fragment:00526.1"
139634. .157494
note="assembly_fragment:02854.0"
157595. .198605
/note="assembly_fragment:03653"
/note="assembly_fragment:03653"
40525 c 41243 g 58791 t 70
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129989. .139533
                                                                                                                                                                                                   104165
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:1"
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/db_xref="taxon:9606"
/chromosome="1"
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198605: cont
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  701 others
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Query Match Best Local Similarity

14.6%;

Score 18; Pred. No.

DB 2; 15;

Length 198605;

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrin, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Ollver, J., Peterson, K., Pierre, N., Roy, A., Santos, R., Schauer, S., Severy, P., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Changer, R., Serbaman, and Talamas, I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 25, 2001 this sequence version replaced gi:8077096.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996–1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, I Young, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                          Summary Statistics
Sequencing vector: M13; M7915; 44% of reads
Sequencing vector: M13; M7915; 56% of reads
Sequencing vector: Dismid: N/a; 56% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 213014 bases at least Q40
Consensus quality: 214764 bases at least Q30
Consensus quality: 214764 bases at least Q30
Consensus quality: 21528 bases at least Q30
Insert size: 210000; agarose-fp
Insert size: 216373; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 218073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 218073)
                                                                                                                                                                                                                                                                                                                                                                                                                   Quality coverage: 10.2 in Q20 bases; agarose-fp Quality coverage: 9.9 in Q20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
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'working draft' sequence. It currently
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133851 151236: contig of 17386 bp in length
151237 151336: gap of 100 bp
151337 174475: contig of 23139 bp in length
174476 174575: gap of
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118767 133750
133751 133850:
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28341. 30420
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/db_xref="taxon:10090"
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421: gap of 100 bp
24529: contig of 1108 bp in length
629: gap of 100 bp
629: gap of 2330 bp in length
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AC079583/c
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                               Consensus quality: 209212 bases at least Q40
Consensus quality: 215597 bases at least Q30
Consensus quality: 215597 bases at least Q30
Consensus quality: 216943 bases at least Q20
Estimated insert size: 212000; agarose-fp estimation
Estimated insert size: 224260; sum-of-contigs estimation
Quality coverage: 10.49 in Q20 bases; agarose-fp estimation
Quality coverage: 9.92 in Q20 bases; agarose-fp estimation
**NOTE: This is a 'working draft' sequence. It currently
** consists of 19 contigs. The true order of the pleces.
** is not known and their order in this sequence record is
                                                                                                                                                                                                                                                    Summary Statistics
                                                                                                                                                                                                                                                                                           Center clone name: RPCI-23_9G1
                                                                                                                                                                                                                                                                                                                Project Information Center Project Name: 1740473
                                                                                                                                                                                                                                                                                                                                                                                                 Center: Joint Genome Institute Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 226060)
DOE Joint Genome Institute.
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown
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208798. .218073
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151337. .174475
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174576. .208697
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46975. .51691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226060 bp DNA HTG 02-SEP-2000 us clone RP23-9G1, WORKING DRAFT SEQUENCE, 19 unordered
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Pred. No.
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14;
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REFERENCE
AUTHORS
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ORGANISM
                                                                                                                      RESULT 3
                                                                                                                                                              Db 174925 GAGGGCTGCACTGACTGG 174908
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                                                                                          ACCESSION
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Best Local S
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                                                                                          Sequence
AX044029
Pizza,M., Hickey,E., Peterson,J., Masignani,V., Galeotti,C., Mora,M
                                                                                                                                                                                                     . Similarity
18; Conserv
                                                Neisseria meningitidis.
Neisseria meningitidis
                                                                                                             AX044029
                                                                               AX044029.1 GI:11342913
                               Neisseria.
                                        Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                               56590
                   (bases 1 to 349980)
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141340
177146
177246
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66697
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29123
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5395
5495
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108 from
                                                                                                                                                                                                                                                           /clone_lib="RPCI mouse BAC 53883 c 54678 g 59093 t
                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-9G1"
                                                                                                                                                                                                                                                                                                                         Location
                                                                                                                                                                                                                                                                                                                                                  54233: gap of unknown length
66596: contig of 12303 bp in le
66696: gap of unknown length
77073: contig of 10377 bp in le
77173: gap of unknown length
97771: contig of 20598 bp in le
97871: gap of unknown length
116093: contig of 18222 bp in le
116193: gap of unknown length
141239: contig of 25046 bp in le
141339: gap of unknown length
147345: contig of 35806 bp in le
                                                                                                                                                                                                                                                                                                                .226060
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                                       beta subdivision; Neisseriaceae;
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j of 5819
 Mora, M.,
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of 3955
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of 4437
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Jof 1498
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g of 1408
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of 5184
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of 9146 bp in length
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of 10582 bp
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Scarselli, M.,
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AUTHORS
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Best Local
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                                                  AY004261.1
                                                                                 AY004261;
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                                                                                                                                                                                          fruit fly.

Drosophila melanogaster

Drosophila melazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Drosophila.
                                                                                                                                                                                                                                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 518)
Davies, R.W., Kaiser, K.U. and Yang, M.Y.
Essential genes and assays relating thereto
Patent: WO 0118547-A 623 15-MAR-2001;
THE UNIVERSITY COURT OF THE UNIVERSITY OF GLASGOW (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scarlato,V., Rappuoli,R., Frazer,C.M. and Grandi,G. Neisseria genomic sequences and methods of their use Patent: WO 0066791-A 108 09-NOV-2000; CHIRON CORPORATION (US); THE INSTITUTE FOR GENOMIC RESEARCH (US)
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AX094499
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                                                                                                               standard;
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                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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/db_xref="taxon:487"
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CELY58G8A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2195 BP; 591'A; 383
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Eukaryota; Alveolata;
Heterocapsa.
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                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                     Caenorhabditis elegans
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AC006808.1 GI:4263130
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                                                                                                                                              Caenorhabditis elegans.
(bases 1 to 34544)
• C. elegans Genome Sequencing Consortium,
nome Sequencing Center, St. Louis U.S.A. a
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/organelle="plastid:chloroplast"
/organism="Heterocapsa pygmaea"
/strain="CCMP 1490"
826. .1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAG25876.1"
/translation="MKNTFNTSNVEANAYSFWGYVIGFILSTSNRLYIGWFGILMFPLL
/LATYAXIAAFIFAPPUDIDGIREPVAGALLYGNNIISGAVIDSSNAIGVHFYPWEAL
GFDEWLYNGGTYQFVVLHFILGAGAYMGREWEFAFRLGMRPWIFVAFSAPLVAASAVFI
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VTSSLVAETAGDLSLNVGYNFGQEDETYSISAAHGYFGRLIFQYASFNNSRSLHFFLAA
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/db_xref="SPTREMBL:Q9MSC1"
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Washington University nd the Sanger Centre,
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                                                                                                                                                                                                                      Direct Submission
Submitted (01-MAR-2000) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (23-FEB-1999) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinxton, U.K.,C. Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998) 99069613
                                                                                                      Submitted
                                                                                                                        University, 4444 Forest
                                                                                                                                       Submitted (28-MAR-2000)
                                                                                                                                                         Waterston, R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tin-Wollam, A.,
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-Wollam, A., Graves, T. and Harrison, M.
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CB10 IRQ, England
e-mail: rw@nematode.wustl.edu
                                                                  Department
                                                                                    Genome Sequencing Center
                                                                                                      by:
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                                                                  Genetics, Washington University
                                                                                                                     Department of Genetics, Park Avenue, St. Louis,
                                                                                                                                                                                                                        Sequencing Center, Washington
4444 Forest Park Parkway, St. Louis,
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Missouri 63108,
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                                                                                                                                                                                                                                                                                                                                    Louis,
                                                                                                                        USA
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neighboring submissions. It may E: This sequence may not be the entire insert of this clone. y be shorter because we only sequence overlapping sections or longer because we provide a small overlap between

and jes@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems This sequence was finished as such as compressions and repeats; all regions
sequence from more than one m13 subclone. problems quality γď

NEIGHBORING COSMID INFORMATION:

This is a segment of the YAC Y58G8, sequenced to span the gap between R02C2 and F33E11. The 5' clone is R02C2, 3100 bp overlap; 3' clone is F33E11, 200 bp overlap. Actual start of this YAC is at base position 20847 of CELDC2; actual end is at 7365 of CELT22H9.

misassemblies, single cloned areas, or regions Sequence fidelity from base pair 6911 to base pair 9100 can not be guaranteed due to a tandem repeat. This region may contain of low quality.

FEATURES source the ing sequences below are predicted from computer
program Genefinder(P. Green and L. Hillier, ms /organism="Caenorhabditis /strain="Bristol N2" /db_xref="taxon:6239" /chromosome="V" Location/Qualifiers analysis, in prepara alysis, using preparation)

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gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains similarity to Pfam family PF00065 (Neurotransmitter gated ion-channel), Score=37.5, E=3.2e-10, N=2; coded for by C. elegans cDNA yk304h6.3; coded for by C. elegans cDNA yk304h6.5; coded for by C. elegans cDNA yk304h6.5; coded for by C. elegans cDNA yk468h10.3; coded for by C. elegans cDNA
                                                                                                                                                                              complement(23241. .24074)
/gene="Y58G8A.4"
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QFCQSLTQKQRSDATSRKKKVNYILIAMVVTFIGLSFYLFFGKKNRSQLF"
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A1SLDKFLH1NDPTKQPVS1RQALA1TFL1W1VSTL1NLPYLMSFEHVDGSFYVQPGE
                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/protein_id="AaF60815.1"
/db.xref="G1:7332128"
/translation="MSAALDEYIRSIFTELYGFLFVLGIFGNGGVLWAVARNKRLQSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E=5.1e-41, N=1)"
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/gene="Y58G8A.3"
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22088. .22244,22429. .22620,22807. .22820))
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/gene="Y58G8A.3"
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EAE I QKEASTS I GISNÞLAESGSDTDLLINLÞKNSEADLSERSETLGMÞDSEKTQKES
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SWKKHCYWGPKGCLDAEPDGNPDWYWSLLEFGITLKRHLPYFSLTIVMPMVSTSLMIL
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/translation="MILLRLISIGVLINFHFGNAASQSTDERKLEAQLLKGYNSKVRP
VKVESTVTQVAVYLNIAHVEKVDEHEQTALVHGHLMASWTDEYLKWERKATNISTLSI
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ITCPRLRANLFDSTVLPALIYGSEAWTFTKELAERVRVTHAALERKLVGLTLTEQRER
NIHREEVREKSKLRDPLIHIKKKKLGWAGHVARRTDGRWTTLMNDWCPRDEKRPVGRP
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VQRLLEVGREYQIPLTUFIDGVKAFDSVEEPQDVWGJLQQGVGYGYINLLQECYTDC
STTFTPFHKNTUPVIRGVRGGDFISPNLESACLEHVFRGLNNKHFKGDERYETEGIS
VNGQNLTNLRFADDIVLVAHNPRTASQMLTELVEKCSSVGLKINTGKTKVLRNRFAYK
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INSFPNGKAAGSDKITADFLKSCGDNVIRLITGRFNRVLESGNIPKDWKTSKTTLIFK
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LANGKFVTDTSVLPSFTNGSDHRLLRSNVHFNINLAKLDQVKRRKPPKRVLEKATALA
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/protein_id="AAF60814.1"
/db_xref="G1:7332127"
/translation="MRKENEKLCTRRGDRNFEETQVSKYKLIIGDFNARVGNRKDENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="Y58G8A"
2379. .5358
/evidence=not_experimental
/product="Hypothetical protein Y58G8A.4"
/protein_id="AAF60816.1"
                                                                                                                                                  complement(join(23241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="contains similarity ot Pfam family PF00001 (7
transmembrane receptor (rhodopsin)), Score=132.4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10191.
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/gene="Y58G8A.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(10191. .10218,10271. .10440,10953. .11104,11151. .1
11346. .11490,11940. .12106,12166. .12319,12367. .12556,
                                                                                                                       /gene="Y58G8A.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome 6, constructed by the Sanger Centre Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                         RP11-320P15 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-10DE6 is at 36226 in this sequence true right end of clone RP1-23916 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        RP11-320P15 is from the library RPCI-11.2 of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
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Jul 19, 2001 this sequence version replaced gi:14329623.
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FDAWLVRRPPFRPFQPQRLPPPSATLSQVIRTMARAFRSLRRLRHKASMILLCKFWVS
WMDFLTYNFQKNLSTFLTTKITISVIVQRSHLFHPKPLERLVLKHFNF"
5567 c 6036 g 10748 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
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/translation="MEIILCFLNYLAHFKAGFEIDLFNFINITIYKKFPFFFHRLKFD
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                                                                                                                                                                                                                                                            /note="MIR repeat:
28243. .28715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369.
                                                   'note="L1MC/D repeat: matches 5528. .5563 of consensus"
                                                                                    /note="L1 repeat: matches 4734. .5064 of consensus"
                                                                                                                            'note="AluY repeat: matches 2.
                                                                                                                                                                'note="MIR repeat:
                                                                                                                                                                                       29991.
                                                                                                                                                                                                      'note="MLT1H repeat: matches 91.
                                                                                                                                                                                                                                       note="L1MA4 repeat: matches 5817. .6300 of consensus"
                                                                                                                                                                                                                                                                                                             /note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                      26081.
                                                                                                                                                                                                                                                                                                                                                'note="MLT1A2 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER89 repeat: matches 8 . .557 of consensus"
21997. .22376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSp repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LTR16C repeat: matches 50.
18546. .18902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9330. .9451
/note="61 copies 2 mer tt 59% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266.
                                                                                                                                                                                                                                                                                                                                                                                      'note="MER57B repeat: matches 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="THE1C repeat: matches 3. .359 of consensus"
16645. .16967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MIR repeat: matches 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="LIM4 repeat: matches 2176, .4208 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC1 repeat: matches 6225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="RP11-320P15"
/clone_lib="RPCI-11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="MER91 repeat: matches 1. .63 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="L2 repeat: matches 2365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="L2 repeat: matches 1035. .2358 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .690. .11001
'note="L1MEC repeat: matches 653. .2052 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="MLT1A1 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="MLT1A1 repeat: matches 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="THE1B repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER20 repeat: matches 160. .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="L1MC1 repeat: matches 5219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MC1 repeat: matches 5883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L1M4 repeat: matches 4735. .4952 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .20635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .19360
 repeat: matches 3821.
                                                                                                                                                                                                                                                                                                                                      26391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 13026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .11442
                                                                                                                                                                                       30151
                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 2665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat:
                                                                                                                                                                matches 28.
                                                                                                                                                                                                                                                                             matches 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     matches 95.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        matches 1432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                matches 1. .364 of consensus"
                                                                                                                                                                                                                                                                                                                 .311 of consensus
                                                                                                                                                                  .186
                                                                                                                                                                                                                                                                             .175 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .184 of consensus"
                                                                                                                              .311 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .221 of consensus"
               .3954 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2700 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2710 of consensus,
                                                                                                                                                                                                                                                                                                                                                 .374 of consensus
                                                                                                                                                                                                      .271 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                      .403 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .426 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .383 of consensus
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                                                                                                                                                                  of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5883 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .6227 of consensus
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                                                                                                                              consensus "
                                                                                                                                                              consensus"
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RESULT 39
SPCC16C4/c
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VERSION
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TITLE
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                                                                                                                                                                                                                       (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome 1 was
sequenced by the Sanger Centre. The sequencing of the S. pombe
genome is now being continued with funding from The European
Commission. Fourteen European sequencing laboratories, including
the Sanger Centre, are participating in the project.
Protein coding regions (CDS) have been predicted with the help of
computer analysis using the Genefinder program in PomBase (an ACEDB
database) with additional predictions for the branch-acceptor sites
supplied by the program Sp3splice. CAUTION: It is possible that for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conser
(complementary strand).
The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.
The length in codons is given for each CDS.
                                                                                             splice donor/acceptor sites.
CDS are numbered using the following system eg
ponnbe), B (chromosome 2), c25H2 (cosmid name),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA, E-mail: barrellesanger.ac.uk and Unite de Biochimie Physiologique, Universite Catholique de Louvain, Place Croix du Sud 2/20, B-1348 Louvain-la-Neuve, Belgium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      staurosporine; tf2 type LTR; TPR Domain; transcription factor subunit; transcription initiation factor tfild 60 kd subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase; G-beta repeats; gene free region; Glucosamine-6-phosphate isomerase; low complexity gene free region; n-terminal acetyltransferase; peptidyl-prolyl cis-trans isomerase; pseudouridylate synthase; RNA binding protein; rna binding protein; rpll2.1; soll family protein; sts5; target of the inhibitor staurosporine; tf2 type LTR; TPR Domain; transcription factor
                                                                                                                                                                           number of introns/exons or we may not have chosen the correct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (03-SEP-1998) European Schizosaccharomyces genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purnelle, B., Goffeau, A., Wood, V., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tission yeast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 44751)
                                                                                                                                                                                                       individual CDS we may have underestimated or overestimated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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32933. .33053
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6661 c 6907 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="L1MC/D repeat: matches 5464. .5553 of consensus" 34424. .34729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="L1M4 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yeast sequencing at the Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44751 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            III cosmid c16C4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 17; pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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13575
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55,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 38225;
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                                                                                               SPBC25H2.01c. SP
.01 (first CDS),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Belgium
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NOT be the entire

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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cosmid c16C4
EM: AL033406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="DPKTLLHGCSKCGSLFIFGRNIKLRTISSERKARTDLKKGEVSR LGTNLEINCLYCSYVHEIPLGVPLRLHGSKQALRAKALAESSSTKLESRKSAHNAKVK ORQRLRASGLNGILDRKKKKDEVAKSTSSLSLQDFMSPI"
join(1000. 1307,1391. .1656,1735. .1796,1877. .2581)
/gene="SPCC1664.01"
complement(join(3019. .3212,3265./gene="SPCC16C4.20c"
                                                                                                       /note="ctaacagatatag, splice branch and acceptor"
complement(join(3019. .3212,3265. .3292,3338. .33
/gene="SPCC16C4.20c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1376. 1390
/note="ctaacattataacag, splice branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MMAVGQLFILRININLQGSVLDSPELMWTEPQLEPIYTAARSYLEINQRVALLNQRVE
VIGDLLSMLKEQITHTHDESLEWIVVILMGLLVLIALFSIVVRLADGFKLNDFRLVIN
NSNKFILLFANTLFYIGGLEAVSITTEESFLFLHYVYIIEEMGKGKKIKPYLSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTYGVVVLWGYTIDEEHRFLRELGRFEIEKLKIEDMEVEEFNYYITTLYQPRIFNDFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTRRMBL:074446"
/translation="MSNRIGPORSTKTAAKLRLLPSTEEFDDFRRQDTGREVYSQIPQ/
LTanslation="MSNRIGPORSTKTAAKLRLLPSTEEFDDFRRQDTGREVYSQIPQ
IEGSTAKROAEHLGKRHEFLLPRVTAACTCDTFRVDLLFKFFQSRRSSHKTRPKQFDE
CIYSPYSYNNEETTDLLPDTLESSRGTLNRESSQESLQSIFEESGLDRNQPLFREVFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="conserved hypothetical protein"
/protein_id="CAA20740.1"
/db_xref="GI:3560255"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(1000. 1307,1391. 1656,1735. 1796,1877. 2581)
/gene="SPCC16C4.01"
/note="SPCC16C4.01"
/note="SPCC16C4.01, len:446, SIMILARITY:Saccharomyces
/note="spcC16C4.01, len:446, similarity:spcC16C4.01, len:446, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAB71193.1"
/db_xref="GI:6855454"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="SPCC16C4.19, len:>140, SIMILARITY:Saccharomyces cerevisiae, RMRP_YEAST, rnase mrp protein component sn (198 aa), fasta scores: opt: 142, E():0.0035, (26.0% identity in 146 aa)"
                                                                                                                                                                                                                                                                                                                                                                                              /note="ttaacatttgtaatttttag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALRDASNYMIRLSISHAIAQSVKISLFEELVNETIDATKDTPQMIAETGRVNLKREEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Schizosaccharomyces pombe"
/strain="972h-"
                                                                                                                                                                                                                                                                           /note="gtatga, splice donor sequence"
1864. .1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="
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/note="SPCC5E4.08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4896"
/chromosome="III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label=SPCC16C4.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /labe1=SPCC16C4.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'gene="SPCC16C4.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "AIII" =qam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fas ta scores: opt: 995, E():0, (54.8% identity in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "nominal overlap with cosmid SPCC5E4, EM:AL033406
chromosome 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtatgc, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gttagt, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   It may be shorter because we only sequence
                                                 .3292,3338. .3349))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acceptor'
                                                                                                                                                              .3349))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            snm1.,
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                   /note="possible gene free region, low complexity, SPCC16C4. 14c and SPCC16C4.15c are predicted in this
                                                                         7366. .7381
7366. .7381
/note="ctaacactatgtgtag,
                                                                                                                                                                                                             /note="Match to PF00639 Rotamase, Score 138.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mSNTGLPKPWIVKISRSRNRPYFFNTETHESLWEPPAATDMAAL
KKFIANELQESVTPTEASNSPKIRASHLLVKHRESRRPSSWKEEHITRSKEEARKLAE
HYEQLLKSGSVSMHDLAMKESDCSSARRGGELGEFGRDEMQKPFEDAAFALKPGEISG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(4510. .6156)
/gene="SPCC16C4.02c"
complement(4510. .6156)
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/note="confirmed intron"
complement(3259. .3264)
                                                                                                                                                                                                                                                                                                                                                                                                                                      VVETSSGFHIIQRHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="peptidy1-proly1 cis-trans isomerase.
/protein_id="CAA20742.1"
/db_xref="GI:3560257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(6836. .7236,7382. .7508)

/gene="SPCC16C4.03"

/note="SPCC16C4.03, len:175, SIMILARITY:Emericella
/note="SPCC16C4.03, len:175, SIMILARITY:Emericella
nidulans, O4273, peptidyl-prolyl cis/trans isomerase.,
(176,aa), f asta scores: opt: 666, E():0, (57.5% identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCECY EVLGLL I RYLCENCDVLAQR I EPDKFFQLQRSLTELFSDTMDFLRDAWDNNKN
RDNLASHVTV I SAVATLCLWLTEDDSQYAQASGLMD I FVYLWRHSWSNG I DYAKWI SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLC IPVICTLSSNPKSAKYLLYYTSF I I NEFPFEQAFEI LSNALYALDNVQTYMRP I F
QGI DKRRGWKLDCTFSFFSDLFSRFPVQSWYSEA I RANLQPLMDAVVERF I TDKNLSS
ATV I LSNLLKAAGPAS I MPNDGFM I LV I GRCSAE I RGSLGMLVKAVGQKGKHGTVSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ttgaccgcgtag, splice branch and
complement(3332. .3337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(3293.
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VERDIQRYRHEAQLLSKVLEKKGLNKEKEAGET"
region, but
                                                                                                                                                                                                                                                                   join(7025. .7236,7382. .7505)
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                              5851. .6943
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Join (6836. .7236,7382. .7508)
/gene="SPCC16C4.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQAIQDFHILIQLNSLVPQSIWNDDIWQEPYWKNLLESNF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPSMLSNKVFFKAFKDFDAWKVVYDDF1KCNDDLKGDKSFNDY1LSTNEEDGEDERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WERMDMKFLDRLLLSTHYEYVDLGVSILLAFCSEEAILRSYEVKKRVSTLLQCCLKHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVTDKDEDSNASGESRGSMELLENCFSLLHAQDDTSKFVSLTMLAKLLNDHPNLIFKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:074447"
/translation="MHIPHFHLHKGPKGVRTISYEQLLSEDDSYASEKLSEDHVTEVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product~"hypothetical protein"
/protein_id="CAA20741.1"
/db_xref="GI:3560256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="gtgtgt, splice d
complement(3293. .3304)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical protein"
/protein_id="CAB71194.1"
/db_xref="GI:6855455"
                                                                                                                                                        'note="gtatgt, splice donor sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SPTREMBL:074448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=SPCC16C4.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=SPCC16C4.02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="SPCC16C4.02c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="SPCC16C4.02c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="gtagga, splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ctaatgaactcgacgtatag, splice branch and acceptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=SPCC16C4.20c
                                                                                                                                                                                                                                                                                                                                                       'note="Match
                                                                                                                                                                                                                                                                                                                                                    to PF00397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .6156)
  SPCC16C4.15c are predicted in very low coding potential and r
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AC020579.5
HTG.
                                                                                 hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit,
                                                                                                                                                                                                                                                                   http://www.tigr.org/softlab/glimmerm_htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the competed extence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280787. Address all correspondence to:at@tigr.org
                                                                                                                                                      similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as
                                            similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST
                                                                                                                                                                                                                                                                                                                                                                                                            prediction programs including Genscan+ (Chris Burge,
http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky,
http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant
of GlimmerM, see Mihaela Pertea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes were identified by a combination of several methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAC clone F1017 is from Arabidopsis thaliana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Town,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-JAN-2000) The Institute for Genomic Research, Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 50821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin,X., Kaul,S., Town,C.D., Benito,M., CreasyT.H., Haas,B.J., Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii;C.Y., Utterback,T.R., Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M. Arabidopsis thaliana chromosome 1 BAC F1017 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin, X. and Kaul, S. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis
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/organism="Arabidopsis thaliana"
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/gene="SPCC164.04"

join(9339. 9601,9647. 9851,9905.

/gene="SPCC16C4.04"
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FDKPGYGESDPDPIRTPKSLALDIEELADQLSLGSKFYVIGKSMGGQAAWGCLKYTPH
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/gene="F1017.2"
13093. .16422
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/gene="F1017.1
/codon_start=1
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/note="identical to heat shock protein 101 GB:AAF26423
/rome | Arabidopsis thaliana| | rom | farabidopsis thaliana| | rom | farabidopsis | faliana| | rom | farabidopsis | faliana| | rom | farabidopsis | farabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(16481. .17251,17318. .17587))
/gene="F1017.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(16481.
/gene="F1017.3"
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/gene="F1017.3"</pre>
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YRVESGGLVDASTGKKSDVLIHIANGPKRSDAAQAVKKMRIEEIEDDDNEEMIED"
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AHVAVFNTLLQVLDDGRLTDGQGRTYDFRNSVI I MTSNLGAEHLLAGLTGKVTMEVAR
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DLRDKLQPLTMKYRKEKERIDEIRRLKQKREELMFSLQEAERRYDLARAADLRYGAIQ
EVESAIAQLEGTSSEENVMLTENVGPEHIAEVVSRWTGIPVTRLGQNEKERLIGLADR
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QQVYVAEPSVPDTISILRGLKEKYEGHHGVRIQDRALINAAQLSARYITGRHLPDKAI
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IFPQAISSAGGENAAQSAERVINQALKKLPSQSPPPDDIPASSSLIKVIRRAQAAQKS
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/gene="F1017.1"
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/gene="F1017.1"
/translation="MAIGPSSVIIIVGIILALTYQSILKPPPPNLCGSPGGPPITAPR
|KLRDGRHLAYKEYGLPREKAKHKIVFIHGSDSCRHDAVFATLLSPDLVQERGVYMVS
                                                                                                           /protein_id="AAG52411.
/db_xref="GI:12324909"
                                                                                                                                                                                                                      /product="unknown protein; 17587-16481"
                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to unknown protein GB:AAD21437 from [Arabidopsis thaliana]"
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/protein_id="AAG52410.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative choline kinase; 11757-10052"
/protein_id="AAG52400.1"
/db_xref="GI:12324898"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="similar to GB:AAC49376 from [Glycine max]"
complement(join(10052. .10159,10243. .10343,10438. .10485,
10576. .10693,10800. .10995,11127. .11248,11404. .11757))
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/db_xref="GI:12324908"
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/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .17587)
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Query Match
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                                                                  /product="putative phosphoribosylformylglycinamidine synthase; 25509-29950"
/protein_id="AAG52403.1"
/db_xref="GI:12324901"
                                                                                                                                                                                                                                                                                                                                                                                              /product="putative ribosomal protein; 23489-24540"
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/protein_id="AAG52401.1"
/db_xref="G1:13234899"
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/translation="MYKGRQGERVRLYVRGTILGYKRSKSNQYPNTSLVQIEGVNTQE
EVNNYKGKRWAYIYKAKTKKNGSHYRCIWGKVTRPHGNSGVVRAKFTSNLPPKSMGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to unknown protein GB:AAD21437
[Arabidopsis thaliana]"
complement(join(21829. .22626,22877. .23197))
/gene="F1017.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown protein; 21119-18687"
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/protein_id="AAG52412.1"
/db_xref="GI:12324910"
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KSMGGQAAWGCLNLKYIPHRLAGVTLVAPVVNYYWRNLPLNVSTEGFNFQQKRDQWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(<23489. .23520,23750. .23785,24176. .24404,24499.
/gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESINRDMIVGFGNWEFGPLDLENPFLNKEGSVHLWQGDEDMLVPAKLQRYLAHQLPWV
HYHEVPRSGHFFHYTKGVVDDIVKSLLTSDVRASRVCI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /t.anslation="MTRDSSRNSSLKPMPRKKFLFPSVVIVIVGIIVAFTYQSKLKPP
PPKLCGSSGGPPITAPRIKLODGRYLAVKEHGLPREKANRKIVE HGSDCCRHDAVFA
TLLSPDLVEELGVYMVSFDRPGYCESDPHPSRFPRSLVSDLEELADQLSLGSKRYVLG
TLSPDLVEELGVYMVSFDRPGVTVAPVVNYXMKNLPLNVSTEGFNFQQKRDQLAVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HES I NRDMIVGFGNWEFDPLDLDNPFLNNEGFVHLWQGDEDMLVPVKLQRYLAHQLPW
VHYHEVPRSGHFFHFTKGVVDNIVTTLLTTDTDT I RQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVAHYAPWLIYWWNTQKWFPGSSIANRDSLLSQSDRDIISKRGYTRKPHWAEVRQQGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(18687..19284,20351..20547,20799.
/gene="F1017.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(join(<18687. .19284,20351.
/gene="F1017.4"</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to ribosomal protein L33B
[Saccharomyces cerevisiae]"
join(23489 _ .23520,23750 . .23785,24176. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown protein; 23197-21829"
/protein_id="AAG52399.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(21829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<21829. .22626,22877. .>23197))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(18687. .21119)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLAGVTLVAPVVNYYWRNLPLNISTEGFNLQQKRDQWAVRVAHYAPWLIYWWNTQNWF
PGSSVVNRDGGVLSQPDKDIILKLGSSRKPHLAEVRQQGIHESINRDMIVGFGNWEFD
                                                                                                                                                                                          join(25509. .25911,25995.
/gene="F1017.7"
                                                                                                                                                                                                                                                                                                                                    29144. .>29950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F1017.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHYTPWLIYWWNTQKWFPGSSIANRDHSLLAQPDKDIISKLGSSRKPHWAEVRQQGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="F1017.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to unknown protein GB:AAD21437 from
[Arabidopsis thaliana]"
                                            translation="MLLQRSSMSQLWGSVRMRTSRLSLNRTKAVSLRCSAQPNKPKAA"
                                                                                                                                                                                                                                                               /gene="F1017.7"
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                                                                                                                                                                                                                               note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="GI:12324897"
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                                                                                                                                                                                                                                                                                                                                                          (<25509.
  13.8%;
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  Score 17;
                                                                                                                                                                                                                                                                                                                                                          .25911,25995. .26563,26663.
                                                                                                                                                                                                                                      GB:KIAA0361 from
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  DB
                                                                                                                                                                                                              .26563,26663.
  8,
Length 50821;
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.29047,29144.
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                                                                                                                                                                                                              .29950)
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KEYWORDS
SOURCE
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
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AC018376
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Best Local Similarity
Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L. Karatas, A., Klein, J., Landers, T., Lehozzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connox, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Stojanovic, N., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J. Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jul 13, 2000 this sequence version replaced gi:6554602. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens, clone RP11-3P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
AC018376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavkly,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boguslavkiy,L., Boukhgaiter,B., Brown,R., Dewari,K., Collins,S., Collymore,A., Cocke,P., Dewari,R., Dewar, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota;
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                                                                                                                                                                                                                                                                                              sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                  However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This record contains 60 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 59935)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L28 Center clone name: 3_P_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center
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                                                                                         916 1015; gap of 100 bp
1016 1921; contid of 00
1921; contid of 00
                                 1921: contig of 906 bp in 1922 2021: gap of 100 bp 2022 2930: contig of 600 bp 2931 3020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Metazoa;
Eutheria;
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Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:K17E12.
AP000381 BA000014
AP000381.1 GI:5672506
               Spermatophyta; Magnoliophyta; oureprophyta; Embryophyta; Tracheophyta; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidoneis 1 (sites)
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Eukaryota; Viridiplantae; Streptophyta;
                                                                                        Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui TAC clone:K17E12.
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9036: gap ontig of 886 t

49922: contig of 886 t

70022: gap of 100 bp

50946: contig of 924 t
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55924: contig of 865
66024: gap of 100 bp
56942: contig of 918 b
7042: gap of 100 bp
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Asamizu, E. and Tabata, S.

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FEATURES
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MEDLINE
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Submitted (28-JUL-1999) Yasukazu Nakamura, Kazusa DNA Research
Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:Ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
Tel:81-438-52-3935, Fax:81-438-52-3934)
Address for correspondence: kaos@kazusa.or.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/),
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://www.sashington.university.School of Medicine, St. Louis,
http://www.sashington.university.School of Medicine, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://genome.wustl.edu/eddy/tRNAscan-SE/).
This sequence may not be the entire insert of this clone. It may shorter because we remove overlaps between neighboring submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c-KI7EL2 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC and BAC clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko, T., Kato, T., Sato, S., Nakamura, Y., Asamizu, E. and Tabata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Res. 7 (3), 217-221 (2000)
20363099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone is MYF5 and the 3' clone is K1G2.
Location/Qualifiers
                                     complement(join(9327. 10950. .11091))
                                                                                                                                                                                                                                                                                                                                                                                                                                     KIVTSEIDQCLNEEFRVIPGLGEFGDRYFGTDE"
complement(join(7607. .7950,8044. .8209))
/note="gene_id:K17E12.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSNSSFSATDDPAAPHOFFVIGVTGGTASGKTTVCDMIIQQLHDHRIVLVNQDSFYRG
LTSEELEHVQEYNFHHPDAFDTEQLLHCVDLIKSGQPVQIPIVDFKTHQRKVDAFRQV
NACDVIILEGILVPHDSFVRDLMNKKIFVDTDADVRLARRIRRDTVERGRDVDSVLEQ
YAKFVKPAFDDFVLPSKKYADVIIPRGGDNHVAVDLIVQHIHTKLGQHDLCKIYPNVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIETTFQIRGMHTLIREKDISKHDFVFYSDRLIRLVVEHGLGHLPFTEKQVVTPTGSV
YSGVDFCKKLCGVSVIRSGESMENALRACCKGIKIGKILIHRDGDNGMQLIYEKLPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="uridine kinase-like protein"
/protein_id="BAB02114.1"
/db_xref="GI:9294212"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(3373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                              /translation="MKMQAVLVILVFSGLLSVKTALAARHVIGGSQGWEQSVDFDSWS
SDQSFKVGDQIELHSVVELGSETAYKSCDLGTSVNSLSSGNDVVKLSKTGTRYFACGT
                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/protein_id="BAB02115.1"
                                                                                                                                                                                                                                                                                                                                                                                                   unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mitsui TAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3702"
/chromosome="3"
                                                                                                                                            VGHCEQGMK I KVNVVSSDSKSASSPSGSGSGSGSGSGSGSGSGSGHGLRASTGYMFVVGS
                                                                                                                                                                                                                                                          /db_xref="GI:9294213"
                                                                                                                                                                                                                                                                                                                                                                     codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MPEDSTAIDYVMEKASGPHFSGLRLDGLLSSPSKSSVSSPSHFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="gene_id:K17E12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SERHVLLLDPVLGTGNSANQAIELLIQKGVPEAHIIFLNLISAPEGIHCVCKRFPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .63604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .ement(join(3373. .3519,3594. .3676,3763. .3835, .4014,4236. .4296,4481. .4541,4626. .4709,4797. .5340,5669. .5765,5900. .6018,6097. .6166,6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 6786))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K17E12"
                                                                        .9715,9806. .9886,10692. .10784,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submissions
CDS
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complement(join(20013. .20129,20428. .20493,20594. .20710
20791. .20862,20950. .21229,21627. .21838,22180. .22239))
//note="gene_id:K17E12.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGQKLILRACEPLPRRRCLAKTYQKQDLSKSPDSLWRSYSNKSYNWSGLGCKSFDCLK
GKKLSKECYGCFDLGVEKDRFYKYKGKNDFLIDDYLGLGSGKIRIGFDISGGSGTFAA
RMAEKNYTYITNTLNNGAPFSEFIAARGLFPLFLSLDHRFPFLDNYFDLIHASSGLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSHSQANSPLLHSSNNISLVSQHLSLILREIDSSQRKLAQMEKQMLGYESIDISRPNI
VPELKLFLQRHQLPLGKDSRTGITEMVSSVGHSCGKSTDLLSQYMSYKVFDRCPDDWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:9294214"
/translation="MGSSSSSLNSPIRADSMVTPESQMTVNDNKNDNVSILSPSVK
KSFESSPKKTSIPANNULTPVKSRWSFSSSKKSFGSKDETFFDSQPWLQSDSDDDFHS
VNGDFTPSLGNTPKSSFSDRPPRFHNLIFHEKKPSRGSSSPAPLPRRKKLGELFRDSI
                                                        VWLVAEEATAAMHCNYQAFTCRVRMQYTWKETXYTKTVPCDVWKMEFGGFAWRLDTTA
                                                                                       ISGEYSPLDQDSLDPSVKSIIGEETQETNTWGMFNGSVTAEMETWVTVESVTSVCEGS
LSSHAVGITDVEIVDNLGKDTCPAFVSDGSNRVVWVNEAYRRNVSGDDSTASVSPEVV
                                                                                                                                            /translation="MDQDDWLGTLRYAGKAQDKVSVDALMLRYRPIAPKPTTGQPCGV
ADNNNNSSYGMSKRTKRKYVRVSKNNKGTCRGKSRSDLSDDREQTDVVTLQLLPEKSD
                                                                                                                                                                                                       /evidence=not_experimental
/protein_id="BAB02120.1"
/db_xref="GI:9294218"
                                                                                                                                                                                                                                                                                                                              similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPGGATAMPKMLNDEAVEYEDGVPATEAQMGKDTVSFLAWAAEPEMEERKLMGFKWTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASCHSMSLISYRDLVGVAYTEEEAKAMAAEIEVVDGPNDEGEMFTRPGKLSDRFPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KADAQVYLSAVLQKPVRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGKAEKLEFLMFDLDRVLKPRGLFWLDNFYCANDEKKKELTRMIERFGYKKLKWVIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
/protein_id="BAB02118.1"
/db_xref="GI:9294216"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="contains similarity to unknown protein
gb|AAB61017.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGYLYFTSGQRDRGPDNPQPGKVIGEMWRTKLKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIIVNNSIVIVGGTTDWHPYTKRLVLVGEIFRFQLDTLTWSVIGRLPYRVKTAMAGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IWRGRLHYMGGSKENRNAVAFDHWSIAVKDGKALDEWREEVPIPRGGPHRACVVANDK
LLVIGGQEGDFMAKPNSPIFKCSRRREIFNGEVYMMDEEMKWKMLPPMPKNNSHIESA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/protein_id="BAB02117.1"
/db_xref="GI:9294215"
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similar to unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                             /note="emb|CAB62340.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YANESAARFANGGAYPPDLSLITKARHNGPNYVFALLTGYRDPPAGISIREGLHYNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSLALLQAAYYRRLKWSVLKSRKLVLDVVN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MGSVSLKIGDGTARFRRTSICSSAVNLLMLFSVVTTNLFALYAF"
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                                                                                                                                                                                                                                                                                                  codon_start=1
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.33512,33590. .33632,33728. .33790,34020. .34090
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5811,16889. .17074,17245. .
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Query Match
Best Local
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Collins, S., Collymore Domino, M., Doyle, M., Forrest, C., Gage, D.,
                        Boguslavkiy,L., Boukhgalter,B., BLOWN,A., COCKE,P., DeArellano,K., Dewar,K., Collins,S., Collymore,A., Cooke,P., DeArellano,K., FitzHugh,W.,
                                                                                     Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F., Boguslavkly,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nomo sapiens
AC018413
                                                                                                                                                                                                                                                                       Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC018413.3 GI:12084068
HTG; HTGS_PHASEO.
                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                           Homo sapiens chromosome, clone RP11-17M16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                  (bases 1 to 65857)
                                                                                                                                                                              (bases 1 to 65857)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISLLHGVSAVVLATNALLSDÞNRGFSSVNTQSQNSILDFSSAYFLADLVHLAVFPSPA
GGDSLFAAHHLAVLFVFLTCRYMVAHGACALLALLVVAEATSACQNTWTLADARGKDA
PLAVSLHRFVTVPFYASYSVCRCVLAPLLIVKMTWFYVSGGADDVIPRMVMVSWTVVI
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GSSEDQSDDAKPMVQGDSSKLVNLQMPETANSEAQRDENTRIDDLFVGSQSTGALEQM
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/translation="mvesaafpggyyrntfeapeesegsgssaqidtevtasensstp
arkcimlnsndedpygvqrqvislynmsqserkdliyrlkleleqtkivlknaelqrm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene_id:K17E12.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(40773. .41084,41393. .41920)
/note="gb|AAC49691.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTAVTVSILWIWNLWVLFFQERYSKFTKKVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence-not_experimental
/protein_id-"BAB02122.1"
/db_xref="GI:9294220"
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unknown protein"
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LYMKQDDGEEEEPEAPVVPKPNETSLERPVDAFGSFNLKGSNPLEQLGLYMKQDDDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGDPERLRKEREELVLQKKKEKARLQAEAEAAEDARRQAEAEAAAEAAEAKRKRELE
REAARQALLKMEKTVEINENSRFLEDLEMLSSSAPEQLPSSAEETSPERPLDALGSFN
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FESSKETWTSTPNITLMKQCDTLLRKLWSHPHSWVFQAPVDVVKLNIPDYLTTIKHPM
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/protein_id="BAB02121.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34154. .34241,34515. .34595,34685. .34794,35165. .35234,
35378. .35520,35718. .36272)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MEPITYSKDLPLFFSIFIFVYLLGYLFIFKKWTPETRPLASSCL"
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3 clone RP11-17M16, LOW-PASS SEQUENCE SAMPLING.
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AUTHORS JOURNAL AUTHORS REFERENCE

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Submitted (10-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 12, 2001 this sequence version replaced gi:9123871. All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pierre, N., Pollara, V., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,G
Karatas,A., Klein,J., Landers,T., Lehoczky,J., Lieu,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This record contains 80 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be generich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved.
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Center clone name: 17_M_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
                                                                                                                           12438 1313
13135 13234:
                            13951: contig
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14052 14777: contiα
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1649 2375: cor
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9822: contig of 729 bp
123 9922: gap of 100 bp
23 10654: contig of 732 bp
5 10754: gap of 100 bp
5 11498: contig of 744 br
11598: gap of
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4044: contig of 7
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5 4964.
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5 5687:
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8149: cor
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12337: cont
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                                                                                                       234: gap of
13951: cont
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gap of 100 br
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18019

15694: gap o

contig of

16505:

17186: con+

18018: cont

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25460 25559: gap of 100 bp 25560 26221: contig of 662 bp in length 26222 26321: gap of 100 bp 26322 27049: contig of 728 bp in length 27050 27149: gap of 100 bp 27150 27186: contig of 737 bp in length 27887 27986: gap of 100 bp 27987 28708: contig of 732 bp in length 28709 28808: gap of 100 bp 29536: contig of 722 bp in length 28809 29536: contig of 728 bp in length 29537 29636: gap of 100 bp 30364 30463: gap of 100 bp 30364 30463: gap of 100 bp 30364 3182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 31182: contig of 719 bp in length 31183 31282: gap of 100 bp 30464 3182 contig of 719 bp in length 31183 31282: gap of 100 bp 30464 3182 contig of 719 bp in length 31183 31282 contig of 719 bp in length 31183 31282 contig of 719 bp in length 31183 31282 contig of 719 bp in length 31183 31283 contig of 719 bp in length 31183 3128
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                                           42649 42748: gap of 100 bp

42749 43483: contig of 735 bp

43484 43583: gap of 100 bp

43584 44321: contig of 738 bp

44322 44421: gap of 100 bp

44422 45147: contig of 726 bp
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18118: gap of 100 bp
18843: contig of 725 bp in length
18943: gap of 100 bp
19668: contig of 725 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           180: gap of 100 bp 40201: contig of 721 bp
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TITLE
JOURNAL
REFERENCE
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AC023633/c
LOCUS
DEFINITION
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KEYWORDS
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      L Unpublished

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E 2 (bases 1 to 65998)

E 3 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Randerson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,

Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,

Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Coske, P.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

DeArellano, K., Dewar, K., Dodge, S., Domho, M., Doyle, M.,

Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Landers, T., Largocque, K., Lebnoczky, J., Levine, R.,

Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,

McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

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McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

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McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

McFwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,

McFwan, P., McGurk, A., McKernan, K., McHernan, R., McMernan, R., McMer
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-287J24
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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HTG; HTGS_PHASE0.
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MCEwan,P., McGurk,A., McKernan,
Meneus,L., Mihova,T., Miranda,(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC023633
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52604 5342: contig of 739 bp in length
53343 53442: gap of 100 bp
53443 54212: contig of 770 bp in length
54213 54312: gap of 100 bp
54313 55040: contig of 728 bp in length
55041 55140: gap of 100 bp
55141 55860: contig of 728 bp in length
55861 55860: contig of 720 bp in length
55961 56702: contig of 742 bp in length
5603 57556: contig of 742 bp in length
5757 57656: gap of 100 bp
57657 57656: gap of 100 bp
57657 58886: contig of 750 bp in length
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58487 59224: contig of
59225 59324: gap of
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tive 0;
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065: gap of 100 bp
46816: contig of 751 bp in length
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100.0%; Pred. No.
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100 bp
of 739 bp in
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40301: 41117:

COMMENT

TITLE

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Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B. Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON JUL 13, 2000 this sequence version replaced gi:6980301. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
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Center clone name: 287_J_24
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Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-149D17
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC027574
AC027574.1 GI:7342319
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      Theodore, J., Tirrel
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Trigilio, J.,
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Submitted (30-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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123
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Copyright (c) 1993 - 2000 Comp
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      AAA81461
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AAA81490
AAH29434
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AAI35723
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                                                                                                                                                                            AAC98121
AAH29882
                                                                                                                                                                                                                                                                                            SUMMARIES
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1039.029 Million cell updates/sec
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Neisseria meningit
N. meningitidis B
Drosophila melanog
Probe #3879 used t
Probe #4282 for ge
Probe #4409 used t
Probe #4170 used t
DNA encoding OMP-1
                                                                                                                                                                                                                                  Description
                                                                                                                                                  Human colon cancer
C albicans apoptos
N. meningitidis pa
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Human CLASP-2 geno	AAC87998	21	567	12.2	15	45
Fusarium venenatum	AAF10271	21	556	•	15	44
secret	AAC01762	21	434	•	15	4 3
Novel human polynu	AAF66405	22	412	•	15	42
Novel human polynu	AAF66301	22	391	•	15	41
human po	AAF66728	22	377	•	15	40
secreted	AAC22215	21	357	•	15	39
Human secreted pro	AAX40689	20	319	•	15	38
Human ORFX ORF451	AAC74896	21	309	12.2	15	37
tamic	AAH67192	22	303	•	15	36
Human gene express	AAZ14187	20	300.	•	15	
Human colon cancer	AAA01492	21	280	•	15	34
O	AAC13255	21	203	•	15	
	AAZ36299	21	201	12.2	15	32
	AAC65362	21	101	•	15	31
	AAV72819	19	101	•	15	30
	AAC65347	21	96	٠	15	29
Tryptophan 2,3-dio	AAV72858	19	96	٠	15	28
Human angiotensino	AAC91627	22	20	12.2	15	27
Human kidney amino	AAX23517	20	50000	٠	16	
Human angiotensino	AAC91677	22	5308	•	16	
-	AAC91676	22	5308	13.0	16	24
Human angiotensino	AAC91675	22	5308		16	
	AAC91674	22	5308	•	16	22
_	AAC91672	22	5308	•	16	
Human angiotensino	AAC91671	22	5308	•	16	20
Human angiotensino	AAC91670	22	5308	•	16	19
Human angiotensino	AAC91600	22	5308	•	16	18
_	AAH33277	22	4201	•	16	17
	AAC78084	21	4201		16	16
Human pancreatic c	AAC98971	21	2732	•	16	15
	AAQ47075	14	1491	13.0	16	14
	AAA38324	21	1278	٠	16	13
Human angiotensino	AAA38323	21	1278	13.0	16	12

ALIGNMENTS

RESULT AAC98121

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09-MAR-2001

(first entry)

AAC98121;

AAC98121 standard; cDNA; 464

ВP

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Human; colon cancer; colon cancer antigen; diagnosis; detection; identification; cytostatic; cardioactive; neuroprotective; vulnes immunomodulatory; muscular; gynaecological; gastrointestinal; nephrotropic; antiinfective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder; ss. WPI; 2000-587534/55. P-PSDB; AAB53364. Rosen CA, (HUMA-) HUMAN GENOME SCI INC 12-MAR-1999; 08-MAR-2000; 2000WO-US05883. 21-SEP-2000 WO200055351-A1 Homo sapiens. Human colon cancer antigen nucleotide sequence SEQ ID NO:131. Ruben SM; 99US-0124270. neuroprotective; vulnerary; renal disorder;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC97991 to AAC98763 encode the human colon cancer associated proteins, CC called human colon cancer antigens, given in AAB53234 to AAB54006. The chuman colon cancer antigens can have cytostatic, cardioactive, muscular; cc human colon cancer antigens can have cytostatic, cardioactive, muscular; cc valuerary, nephrotropic, antiinfective and antibacterial activities, and CC can be used in gene therapy. The colon cancer antigen polynucleotides, cc proteins and antibacies to the proteins are useful for the prevention, cc treatment and diagnosis of colon disorders, such as colon cancer. The CC polynucleotides may be used in diagnostics and research, such as for CC chromosome identification, and as hybridisation probes. The proteins CC may also be used to prevent diseases such as neural disorders, immune c system disorders, muscular disorders, reproductive disorders, infectious CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and CAAB54007 represent sequences used in the exemplification of the present of overlation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 18
                              disorders, yeast certain diseases
                                 Yeast and fungal nucleic acids encoding proteins involved in a pathway leading to programmed cell death, useful for treating proliferative disorders, yeast and fungal infections, or for preventing apoptosis in certain diseases .
                                                                                                                                               Nelissen
                                                                                                                                                          Contreras RH,
                                                                                                                                                                                     (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                  01-JUL-1999;
                                                                                                                                                                                                                                            03-JUL-2000; 2000WO-BE00077
                                                                                                                                                                                                                                                                        11-JAN-2001
                                                                                                                                                                                                                                                                                                 WO200102550-A2
                                                                                                                                                                                                                                                                                                                            Candida albicans
                                                                                                                                                                                                                                                                                                                                                        vaccine;
                                                                                                                                                                                                                                                                                                                                                                     Yeast; fungus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH29882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH29882 standard; DNA; 1303 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                                                                                                                                                                                                                                                                                albicans apoptosis associated coding sequence #26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agatgccttacaaccctg
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                                                                                                                 2001-367042/38.
     17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer associated gene sequences, referred to ens, useful for the treatment, prevention, and
                                                                                                    AAG70846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                        autoimmune
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  Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
    2
                                                                                                                                                                                                                                                                                                                                                       apoptosis; infection; proliferative disease;
mmune disease; ischaemia; neurodegeneration;
                                                                                                                                            De Backer MD,
Reekmans RJ;
                                                                                                                                                                                                                99EP-0870141
    218pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 18;
Pred. No.
                                                                                                                                                         Luyten WHML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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diagnosis of co
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RESULT AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB1461 ID AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AAAB16CC AABA16CC AAAB16CC AABA16CC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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                                     The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82144 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB25663 represent Neisseria DNA sequences and their corresponding proteins; AAA81254 to AAA81304 and AAA81312 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81259 and AAA81304 to AAA81312 represent PCR primers used in the isolation of Neisseria meningitidis DNA sequences; and AAA81322 to AAA81452 represent Neisseria meningitidis MenB polynucleotide ORF sequences, which are all used in the exemplification of the present invention. The nucleic acid sequences, protein sequences, and antibodi against them, can be used in the manufacture of a composition. The
                                                                                                                                                                                                                                                                                                                                   Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of apoptosis associated proteins from the yeast Saccharomyces cerevisiae and the fungus Candida albicans. These can be used to identity treatments for fungal and yeast infections, for proliferative diseases and for apoptosis related diseases such as autoimmune diseases, ischaen and neurodegeneration. The present sequence is one of the C. albicans
composition medicament)
                                                                                                                                                                                                                                                                                                                                                                                other Neisserial infections,
                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection \boldsymbol{a}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-318079/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frazer CM, I
Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1998;
30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rappuoli R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-2000.
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                                                                                                                                                                                                                                                                                                                                   Page 326-329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine;
                        can
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99US-0132068
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be used as a medicament
treating, preventing or
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C, Mora
                                                                                                                                                                                                                                                                                                                                 1760pp;
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                                                                                                                                                                                                                                                                                                                                   English
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Ratti G,
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                                                                  he present and antibodies
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08-OCT-1999;
28-FEB-2000;
sequences which overlap each other at the beginning and end of each sequence by 49980 bp (i.e. the last 49980 bp of AAF21544 is repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated the beginning of AAF21608, and so on). AAF21545 to AAF21588 encode the
                                                                                                  The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 represent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequence was too long to go in a record on its own it was split into 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             be components of vaccines against Meningococcus B; against all serotypes and/or against all pathogenic Neissariae. Identification of sequences from the bacterium will also facilitate production of biological probes, particularly organism-specific probes. Attempts to make efficacious Meningococcus B vaccines have failed mainly due to antigen tolerance. Multivalent vaccines have also been tried but none have successfully overcome antigenic variability. The provision of further, complete sequences may provide an opportunity to identify secreted or surface exposed proteins that may be presumed targets for the immune system and which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pizza M, Hi
Galeotti C,
                                                                                                                                                                                                                                                     Claim 7;
                                                                                                                                                                                                                                                                                                     Neisseria meningitidis B full length frames are used to detect, treat and
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-647603/62
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                                                                                                                                                                                                                                               Appendix A;
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C, Mora M,
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Ratti G, (
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Scarlato V,
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                                                                                                                                                               WPI;
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30-APR-1999;
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                                                                                                                                                                                     Rappuoli R,
                                                                                                                                                                                                Masignani V,
                                                                                                                                                                                                             Frazer CM,
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99US-0132068
                                                                                                                                                                                                                                                                                             99WO-US23573
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diagnosis; infection; antibacterial; identificat
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                                                                                                                                                                                                Peterson
C, Mora
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                                                                                                                                                                                                                                                                                                                                                                                                                                      genome DNA sequence
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The present invention describes methods of obtaining immunogenic proteins from Neisseria genomic sequences. AAA81453 to AAA82414 represent specifically claimed Neisseria meningitidis genomic DNA sequences; AAA81260 to AAA81303 and AAB25620 to AAB2563 represent Neisseria DNA sequences and their corresponding proteins; AAA81254

Neisseria DNA sequences and their corresponding proteins; AAA AAA81259 and AAA81304 to AAA81321 represent PCR primers used isolation of Neisseria meningitidis DNA sequences; and AAA813

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Isolated nucleotide sequences of Neisseria meningitidis which can used in the diagnosis and treatment of N. meningitidis infection ϵ other Neisserial infections, for example, N.gonorrhoea -

infection and

Claim 7; Page 866-1272; 1760pp; English

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CC sequences, which are all used in the exemplification of the present
CC invention. The nucleic acid sequences, protein sequences, and antibodies
CC composition can be used in the manufacture of a composition. The
CC composition can be used as a medicament (or in the manufacture of a
CC medicament) for treating, preventing or diagnosing infection due to
CC Neisserial bacteria. For example, some of the identified proteins could
CC be components of vaccines against Meningococcus B; against all serotypes;
CC and/or against all pathogenic Neissariae. Identification of sequences
CC from the bacterium will also facilitate production of biological probes,
CC particularly organism-specific probes. Attempts to make efficacious
CC Multivalent vaccines have failed mainly due to antigen tolerance.
CC Multivalent vaccines have also been tried but none have successfully
CC overcome antigenic variability. The provision of further, complete
CC sequences may provide an opportunity to identify secreted or surface
CC exposed proteins that may be presumed targets for the immune system and
CC which are not antigenically variable or at least more conserved than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                The present sequence is part of an essential gene from Drosophila melanogaster. Lack of expression of the protein encoded by this gene leads to a lethal or semi-lethal phenotype. The invention relates to 902 nucleic acid sequences from genes encoding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
which are thought to be essential, and to a screening assay for identifying compounds which have a physiological effect on these proteins. Suitable compounds are useful as pesticides and may be in conjunction with other pesticides and herbicides for crop
                                                                                                                                                                                                                                                                                                                                                                               Screening assa
physiological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila pesticide;
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18; Conser
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Pred. No.
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Best Local :
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26-MAY-2000;
30-JUN-2000;
                                                                          The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the problem hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the human breast of the beautiful the proposition of development.
                                                       of the breast, fibrocystic non-carcinoma tumours.
                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                           04-OCT-2000
                                                                                                                                                                                                                                                                                                                       21-SEP-2000;
27-SEP-2000;
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                                  specification,
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                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                  SG,
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                                 The sequence data for this patent did not fication, but was obtained in electronic for
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17; Conservative
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                                                                                                                                                                                   SEQ ID No
                                                                                                                                                                                                                                                                Hanzel DK,
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2000US-0234687.
2000US-0236359.
2000US-0024263.
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2000US-0207456.
2000US-0608408.
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                                                                  changes, proliferative breast
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Query Match

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Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                                                                                                      expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                       Sequence
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27-SEP-2000;
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03-AUG-2000;
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26-MAY-2000;
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                     31 ccctgatgacctaatg
                                                                                      Local Similarity 100.0%; es 16; Conservative
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CCCTGATGACCTAATG
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RESULT 9 AAI35723/c

WO200157270-A2

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RESULT 10
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to single exon nucleic acid probes The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes at for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                  09-OCT-2001
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26-MAY-2000;
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                                                          Homo sapiens.
                                                                                                Probe; human;
inflammatory o
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16; Conserv
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2000US-0236359.
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Matches 16
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours.
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    (OHIS ) UNIV OHIO STATE
                         19-SEP-1997;
                                                                  25-MAR-1999
                                                                                       WO9913720-A1
                                                                                                            Ehrlichia chafeensis
                                                                                                                                 detection;
                                                                                                                                            Outer membrane
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                                                                                                                                                                                                            AAX34755;
                                                                                                                                                                                                                               AAX34755 standard;
                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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27-SEP-2000;
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2000GB-0024263.
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Pred. No.
                                                                                                                                           Ehrlichia chafeensis;
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RESULT 12
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Best Local
                                                                          Assessing cardiovascular status in humans involves comparing polymorphic pattern comprising polymorphic positions within encoding specific proteins, with reference polymorphic pattern.
                                                                                                                  WPI;
                                                                                                                                                                            14-OCT-1998;
14-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention provides isolated outer membrane proteins (OMP) from Ehrlichia chafeensis and E. canis. The E. chaffeensis proteins form part of the OMP family and consist of proteins OMP-1, -1(B to Z) shown in AAV06943-958. The E. canis proteins form part of the P30 family and consist of proteins shown in AAV06959-970. The proteins and genes are used to detect E. chaffeensis in patients and E. canis in dogs.
                                                        Disclosure;
                                                                                                                                                                                                                                                                                              polymorphic marker; cardiovascular disease; myocardial unstable angina; hypertension; atherosclerosis; stroke
                                                                                                                                    Norberg
                                                                                                                                                                                                         13-OCT-1999;
                                                                                                                                                                                                                            20-APR-2000
                                                                                                                                                                                                                                               W0200022166-A2
                                                                                                                                                         (EURO-)
                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                     screening;
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                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                         MEDICAL
                                                                                                                                                                            98US-0104286
98US-0104302
                                                                                                                                                                                                         99WO-IB01678
                                                                                                                                                                                                                                                                                     ; hypertension; atherosclerosis; stroke; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                                                  gene; AGT; regulatory region; polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295
                                                      126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55pp;
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Pred. No.
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                                                                                                                                                                                                                                                                                             infarction; prognosis;
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The invention relates to a novel method of assessing the cardiov status in an individual and to newly identified polymorphisms in genes encoding angiotensin-converting enzyme (ACE), angiotensin receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), r

beta-adrenergic

(AGT), renin

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RESULT 13
AAA38324/c
ID AAA383
XX AAA383
XX 21-AUG
DT 21-AUG
DX Human
XX Angiot
KW Angiot
KW Polymc
KW Unstab
KW Unstab
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Best Local :
                                              13-OCT-1999;
                                                                                                                                                                                                                                            Angiotensinogen gene; AGT; coding region; polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis;
    14-0CT-1998;
                                                                                                                                                                                                                                                                                                                                       Human angiotensinogen (AGT) gene exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA38324 standard; DNA; 1278
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                                                                                           20-APR-2000
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                           drug screening;
                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-2000 (first entry)
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mes 16; Conserv
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    98US-0104286
                                              99WO-IB01678
                                                                                                                                                                                                                           treatment outcome;
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AAQ47075;

AAQ47075 standard;

DNA; 1491 BP

13-JAN-1994

(first entry)

δÃ Вþ

522 TGGTAAGTTTCACATG 71 tggtaagtttcacatg

507 86 Matches Query Match Best Local

16;

Conservative

Similarity

13.0%; put 100.0%; Pr --- 0;

Score 16; Pred. No.

DB 26

0;

Indels

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Gaps

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21; Length 1278;

Sequence 1278

BP;

283

A;

343

Ç 295 <u>.</u> 357

Η,

0

other

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CC Fragments of the genes comprising a polymorphic site may be used as CC primers and probes for detecting genetic polymorphisms or in molecular CC library arrays for high throughput screening. The genes, and the proteins CC they encode are useful in the screening of potential cardiovascular CC drugs. Determination of an individual's polymorphic pattern reduces or CC eliminates trial and error in selecting a treatment for a particular CC individual cardiovascular patient. It also provides the ability to CC eliminate patients from clinical trials who are predicted to be CC individual cardiovascular patient. It also provides the ability to CC eliminate patients from clinical trials who are predicted to be CC individual cardiovascular patients in an early trial can be evaluated to increasinent regimen. Adverse results in an early trial can be evaluated to CC identify polymorphic patterns so that the adverse results can be CC correlated with a sub-population of the test population, permitting CC exclusion of such sub-populations from the treatment group. Beneficial CC drugs can be approved for use in the appropriate population, thereby CC currents of the duration and cost of such trials. Sequences A38324 cc A38327 represent exons 2, 3, 4 and 5 of the human angiotensingen gene CC coding region (GenBank M24686-M24689). The polymorphic sites identified CC at mostifion 49 in exon 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pattern of polymorphisms from the individual with a reference polymorphi pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a pattent given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-arenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aldosterone synthase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EURO-) EURONA MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andersson MK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0104302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AGT), renin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polymorphic
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antigen

DNA

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RESULT 1
AAC98971/
ID AAC9
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AC AAC9
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AC AAC9
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Huma
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Huma
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Human; pancreas; pancreatic cancer; pancreatic cancer antigen; detection; diagnosis; identification; cytostatic; neuroprotective; nootropic; immunomodulatory; relaxant; contraceptive; gynaecological; antiinflammatory; cardiant; gene therapy; chromosome mapping; linkage analysis; tissue identification; tissue typing; forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5. This sequence was isolated by PCR using the primers given in AAQ47068-72. Primer 21B4 corresponds to part of the repeated region of 21B4/rhoptry antigen. In hybridisation assays this primer recognised two trandemly repeated regions suggesting that B bovis contains two copies of the 21B4/rhoptry antigen gene. The two proteins encoded by the two antigen genes are identical. Primers 21B4.2 and 21B4.3 flank the 21B4-309 cooling region of the antigen gene. Primer 21B4.4 primes synthesis just 3 to the end of the open reading frame. The entire open reading frame was shown to encode five antigen genes. The 3 non-repetitive sequences of open reading frame to the open reading frame. Babesia antigen genes can be used in the production of a combined vaccine which will stimulate a greater immune
                                                                                                                                         09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting closely linked gene copies which encode protective antigen against babesiosis - by screening babesial genomic DNA library with oligo-nucleotide probe based partial sequencing of protective antigen and identifying positive clones
                                                                                                      Human pancreatic
                                                                                                                                                                                                        971/c
AAC98971 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the Babesia bovis 21B4/rhoptry antigen 5. This sequence was isolated by PCR using the primers given it AAQ47068-72. Primer 21B4.1 corresponds to part of the repeater region of 21B4/rhoptry antigen. In hybridisation assays this part of the repeater of the repeater region of 21B4/rhoptry antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymerase chain reaction; PCR; amplify; primer; detection; babesiosis; parasite; Babesia bovis; 21B4/rhoptry; antigen; repeat region; immune response; vaccine; ss.
                                                                                                                                                                           AAC98971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dalrymple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JUL-1993
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                                                                                                                                                                                                                                                                                               941 cttacaaccctgatga
                                                                                                                                                                                                                                                                                                               24 cttacaaccctgatga
                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and afford broader immunity than a single antigen vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽,
                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
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                                                                                                     cancer antigen nucleotide sequence SEQ ID NO:199
                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 A; 286
                                                                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                   13.0%;
100.0%;
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26;
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AAC78084/c
ID AAC780
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AC AAC780
AC AAC780
DT 08-FEE
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DE Human
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KW Human;
KW diagnc
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC98773 to AAC99231 encode the human pancreatic cancer associated proteins, called pancreatic cancer antigens, given in AAB54008 to AAB54466. The human pancreatic cancer antigens have cytostatic, neuroprotective, nootropic, immunomodulatory, relaxant, contraceptive, gynaecological, cardiant and antiinflammatory activities, and can be us in gene therapy. The polynucleotide and proteins can be used for preventing, treating, or ameliorating a medical condition or in assays for diagnosing a pathological condition or a susceptibility to one in a subject. Binding partners to the proteins and the activity of the proteins can be identified. The pancreatic cancer antigens can be used detect, treat or prevent pancreatic disorders, especially cancer.

Agonists and antagonists to the antigens can be screened for. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pancreatic cancer antigen polynucleotides can be used to design nucleic acid hybridisation probes that can be used in chromosome mapping, linkage analysis, tissue identification and/or typing and a variety of forensic and diagnostic methods. The proteins can be used to generate antibodies which are used to purify, detect and target the polypeptides, including both in vivo and in vitro diagnostic and therapeutic methods. The proteins can be used to treat or prevent neural, immune system, muscular,
                                                                                       08-FEB-2001
                                                                                                                          AAC78084;
                                                                                                                                                             AAC78084 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                         reproductive, gastrointestinal, pulmonary, cardiovascular, renal or proliferative disorders. AAC99232 to AAC99240 and AAB54467 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a pancreatic cancer antigen for preventing, treating, or ameliorating a medical condition, particular pancreatic cancer, or for use in assays for diagnosing a pathological condition
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2732 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 645-646; 1379pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neural; immune system; muscular; reproductive; gastrointestinal;
pulmonary; cardiovascular; renal; proliferative; ss.
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                                                                                                                                                                                                                                                                                                                                     Local
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DB; AAB54206.
                                                                                                                                                                                                                                                                                                                    Similarity 100. 16; Conservative
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                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          624 A; 753 C;
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                                                                                                                                                                                                                                                                                                               100.0%; *.
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                                                                                                                                                                                                                                                                                                                                                     Length 2732;
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diagnosis;

cytostatic;

associated gene; cancer tostatic; proliferative;

antigen; de vulnerary;

detection;

0

immunomodulator;

Human cancer associated gene sequence SEQ ID NO:478

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RESULT 17
AAH33277/c
ID AAH332'
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AC AAH332
XX
DT 03-SEP
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Best Local
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                    03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                        Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                       AAH33277;
                                                                                         AAH33277 standard;
                                                                                                                                                                                  2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel isolated nucleic useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                   N
                                                                                                                                                                                                                                                                                                                                                                             present invention
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                                                                                                                                                                                AGGTATTGTAAATGTG
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16; Conser
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                                                                                                                                                                                                                                                                                                                                              4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC78448 encode the human cand to AAB44239. The proteins can
                                                                                                                                                                                                                                                      Conservative
                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                            BP; 1323 A;
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                                                                                         cDNA; 4201 BP
                                                                                                                                                                                                                                                                     13.0%;
                                                                                                                                                                                2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acids comprising sequences encoding peptides
                                                                                                                                                                                                                                                                                                                                            637
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Pred. No.
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25;
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16-MAR-2001 AAC91600

(first

entry)

AAC91600 standard; DNA; 5308

ВP

Human angiotensinogen

Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screening;

gene 5' region/exon 1, SEQ ID NO:1.

밁 Qy

N

2555 AGGTATTGTAAATGTG 2540

aggtattgtaaatgtg 17

0,

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Query Match
Best Local
Matches
                                                                                                                                                                           the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                             N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                             AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human cancer-associated nucleic acid molecules (N) and proteins (P),
                                                                                Sequence 4201 BP; 1323 A; 637 C; 850 G; 1381
                                                                                                                                                               present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben
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03-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal carcinoma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 2445-2447;
 16;
             Similarity
 Conservative
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99US-0163280.
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                 100.0%;
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               Score 16;
Pred. No.
red. No. 25;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                Length 4201;
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AC AAC9:
XX
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                                                                                                                                                                                                                                                                                                                                                                                                  CC mutant alleles of which cause a susceptibility to insulin dependent CC diabetes meallitus (IDDM, type I diabetes). The AGT gene is located CC on chromosome 1942-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene CC (AAC91600-C91604) and a genomic sequence comprising an alternative AGT CC gene exon 1 (AAC91606). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the CC mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC methods of screening for drug candidates which may be useful in the CC treatment of diabetes resulting from an AGT mutation. Methods of CC reventing or treating diabetes are claimed which comprise the CC administration of a compound which agonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises or antagonises wild-type or inhibits AGT gene expression, or which cleaves AGT proteins. In addition, CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, CC inhibits AGT modulators can be used to treat or prevent diabetes. Mutant CC AGT proteins or fragments thereof are useful for screening compounds of the compounds of the compounds thereof are useful for screening compounds.
                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                     2311
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                 16-MAR-2001
                                                   AAC91670;
                                                                                  AAC91670 standard;
                                                                                                                                                                                                                                                                                                                       Sequence 5308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to the human angiotensinogen (AGT) gene, some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1999; 99US-0135423
06-JAN-2000; 2000US-0174700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-2000; 2000WO-US13327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                   71 tggtaagtttcacatg 86
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                  TGGTAAGTTTCACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-025172/03
                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                     Similarity 100
l6; Conservative
                                                                                                                                                                                                                                                                                                                                                                           of the human
                                                                                                                                                                                                                                                                                                                                                                    to AGT polypeptides. The present sequence represents a {\bf f} the human AGT gene comprising part of the 5' region a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Russell DL,
               (first entry)
                                                                                                                                                                                                                                                                                                                      BP; 1364 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0135423.
                                                                                  DNA; 5308 BP
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                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83pp; English.
                                                                                                                                                                   2296
                                                                                                                                                                                                                                                                      13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shattuck DM;
                                                                                                                                                                                                                                                                                                                       1265 C; 1329 G; 1350 T;
                                                                                                                                                                                                                                                   Score 16;
Pred. No.
                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                    22;
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                                                                                                                                                                                                                                                                                                                       0 other
                                                                                                                                                                                                                                                                                                                                                                     region and
                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                         exon
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밁 δÃ

2311

71 tggtaagtttcacatg 86

Matches Query Match Best Local :

16;

Conservative

0;

Mismatches

0;

0,

Gaps

0

Similarity

RESULT

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The invention relates to the human angiotensinogen (AGT) gene, some mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type I diabetes). The AGT gene is located on chromosome 142-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91884, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the
                                                                                                                                                                                     inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line derived therefrom, comprising a mutant human AGT allele. The polymorphisms identified in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon
                                                                                                                                                                                                                                                                                                                                                                                   treatment of diabetes resulting from an AGT mutation. Methods of preventing or treating diabetes are claimed which comprise the administration of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which
                                                                                  Sequence
                                                                                                                                                   derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page -; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus usen
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06-JAN-2000; 2000US-0174700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeniantidiabetic; gene therapy; 5' region; mutant; exon 1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McGrail M,
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                                                                                                                             : The present sequence is not shown in the specification, but is
from the wild-type human AGT gene 5' region/exon 1 sequence
n page 60-63.
                                                                                  5308 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Russell DL,
                                                                                     1364
13.0%;
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                                                                                  A; 1264 C; 1329 G; 1351 T; 0 other,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' region mutant,
Score 16;
Pred. No.
25,
                    22;
                 Length 5308;
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AAC91671/c

ID AAC91671;

XC AAC91671;

XC AAC91671;

XX 16-MAR-2001 (first entry:
XX 21-MAR-2001 (first entry:
XX Human angiotensinogen gene
XW Human angiotensinogen gene
XW Human angiotensinogen gene
XW Human angiotensinogen gene
XW Human angiotensinogen gene
XW Homo sapiens.
YX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX Homo sapiens.
PM W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX Clamay-2000; 2000WO-US133:
YX Z1-MAY-2000; 2000WO-US133:
YX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX Clamay-2000; 2000WO-US133:
YX Z1-MAY-2000; 2000WO-US133:
YX W0200071751-A1.
XX W0200071751-A1.
XX W0200071751-A1.
XX Clamay-2000; 2000WO-US133:
YX W0200071751-A1.
XX Clamay-2000; 2000WO-US133:
YX Claim 2: Page -: 83pp: En.
XX Wovel angiotensinogen general interestion of which concurrence interestion of which concurrence interestion of acquency concurrence for characted to IDDM; detecting mutant are related to IDDM; detecting muta
                                                             cc mutant alleles of which cause a susceptibility to insulin-dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1942-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also CC relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC methods of screening for drug candidates which may be useful in the CC administration of a compound which agonises or antagonises wild-type or CC mutant AGT, which agonises or antagonises wild-type or CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line CC polymorphisms identified in the AGT gene are useful for determining if a method bind to AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for cereening compounds CC which bind to AGT polypeptides. The present sequence represents a portion CC in the human AGT gene comprises on the wild-type human AGT gene 5' region/exon 1 sequence CC shown on page 60-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for diagnosis of predisposition to diabetes -
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06-JAN-2000; 2000US-0174700
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               5308 BP; 1364 A; 1266 C;
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               1329
           G; 1349
               T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug screening;
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Best Local Similarity 100 Matches 16; Conservative

13.0%; 5c. 100.0%; Pr/ 0;

Score 16; Pred. No.

25; 22; 0

Length 5308;

Indels

0;

Gaps

0

shown on

Mismatches

Query Match Best Local

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                                                                                                                                                         The invention relates to the human angiotensinogen (AGT) gene, some CC mutant alleles of which cause a susceptibility to insulin-dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1q42-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising an alternative AGT CC (AAC91600-C91604) and a genomic sequence comprising an alternative AGT CC (AAC91600-C91604). The invention also encompasses the specifically CC mutant angiotensinogen proteins AAB48945-B48949. The invention also CC relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC developing diabetes resulting from an AGT mutation. Methods of creening for drug candidates which may be useful in the CC treatment of diabetes resulting from an AGT mutation. Methods of correction of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which comprises an AGT genes and CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line correct has or is at triky from downland animal, or cell line derived therefrom, comprising a mutant human AGT allele. The
             person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon 1. Note: The present sequence is not shown in the specification, but is derived from the wild-type human AGT gene 5' region/exon 1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 142-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeni antidiabetic; gene therapy; 5' region; mutant; exon 1; ds.
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AAC91672 standard; DNA; 5308
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06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shattuck DM;
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Sox

Sequence 5308 BP; 1364 A; 1264 C; 1329 G; 1351 T; 0 other;

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The invention relates to the human angiotensinogen (AGT) gene, some CC mutant alleles of which cause a susceptibility to insulin dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1942-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene CC (AAC91600-C91604) and a genomic sequence comprising an alternative AGT CC gene exon 1 (AAC91606). The invention also encompasses the specifically CC claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the CC mutant angiotensinogen proteins AAD84945-B48949. The invention also CC relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC developing diabetes via detection of a polymorphism in the AGT gene; and CC methods of screening for drug candidates which may be useful in the CC preventing or treating diabetes are claimed which comprise the CC administration of a compound which agonises or antagonises wild-type or mutant AGT, which agonises or antagonises an AGT receptor, which comprising a mutant human animal, or cell line CC inhibits AGT gene expression, or which cleaves AGT proteins. In addition, CC the invention encompasses a transgenic non-human animal, or cell line CC polymorphisms identified in the AGT gene are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes
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AAC91674/c
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06-JAN-2000; 2000US-0174700
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RESULT 2
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Best Local
                        discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91605). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the
                                                                                                                                                                       mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located on chromosome 1q42-43, a region linked to IDDM. The invention
                                                                                                                                                                                                                                                                                   Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus usef diagnosis of predisposition to diabetes -
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2311 TGGTAAGTTTCACATG 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGT proteins or fragments thereof are useful for screening compoundable bind to AGT polypeptides. The present sequence represents a of the human AGT gene comprising a mutant 5' region fragment, and 1. Note: The present sequence is not shown in the specification, derived from the wild-type human AGT gene 5' region/exon 1 sequence shown on page 60-63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeni
treatment of diabetes resulting preventing or treating diabetes
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                                                                                                                                                                                                                                                        Claim
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06-JAN-2000; 2000US-0174700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant
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RESULT 24
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XX Human
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The invention relates to the human angiotensinogen (AGT) gene, some mutant alleles of which cause a susceptibility to insulin-dependent diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located on chromosome 1q42-43, a region linked to IDDM. The invention discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT gene exon 1 (AAC91606). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the
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Best Local
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AAC91677
                                                                                                              Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful diagnosis of predisposition to diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 person has, or is at risk from developing insulin-dependent diabetes mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant AGT proteins or fragments thereof are useful for screening compounds which bind to AGT polypeptides. The present sequence represents a portion of the human AGT gene comprising a mutant 5' region fragment, and exon 1. Note: The present sequence is not shown in the specification, but is derived from the wild-type human AGT gene 5' region/exon 1 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutant AGT, which agonises or antagonises an AGT receptor, which inhibits AGT gene expression, or which cleaves AGT proteins. In addition, the invention encompasses a transgenic non-human animal, or cell line derived therefrom, comprising a mutant human AGT allele. The polymorphisms identified in the AGT gene are useful for determining if a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            relates to detecting mutant AGT alleles or gene products thereof which are related to IDDM; determining whether a person has, or is at risk of developing diabetes via detection of a polymorphism in the AGT gene; and methods of screening for drug candidates which may be useful in the treatment of diabetes resulting from an AGT mutation. Methods of preventing or treating diabetes are claimed which comprise the administration of a compound which agonises or antagonises wild-type or
                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1999;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDDM; SNP; diagnosis; susceptibility; transgenic ani antidiabetic; gene therapy; 5' region; mutant; exon
                                                                                                                                                                                                                                                                                                McGrail M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAY-2000; 2000WO-US13327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1q42-43; single nucleotide polymorphism; IDDM; SNP; diagnosis; susceptibility; transgenic animal; drug screeni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5308 BP; 1364 A;
                                                                                                                                                                                                                                                                                                                                                           (MYRI-) MYRIAD GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human angiotensinogen gene 5' region mutant, G2829A
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                                                                                                                                                                                                                                                                                                Russell DL,
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2000US-0174700
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The invention relates to the human angiotensinogen (AGT) gene, some

Claim 2; Page -; 83pp;

English.

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RESULT 26
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                                  WPI; 1999-205193/17
                                                                                                     (MEDI-) MEDICAL COLLEGE GEORGIA RES INST
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                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                       arterial
                                                                                                                                                                                                                                                                                                                                                  Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency; prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                      Human kidney
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                                                                                                                                                                                                                                                                                                                                       stenosis;
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                                                                   Sprinkle TJC,
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encoding

human

aminopeptidase P

Example 2;

Page 33; 83pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also used to identify Amp-expressing sequences in other animals and to generate transgenic animals, and comparisons of genemic sequences are used to detect mutations. Amp inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis or atherosclerosis. The structure of Amp is used to design synthetic substrates, e.g. for use in Amp assays. Amp, which hydrolyzes N-terminal imido bonds, can be used to degrade industrial protein feeds to free amino acids, to degrade proteinaceous wastes, as additives in enzyme formulations used to treat malabsorption syndrome and for studying its biological role. Antibodies against Amp are used in immunohistochemical methods to study Amp distribution.
                                            Novel angiotensinogen gene, mutant alleles of which causes susceptibility to insulin-dependent diabetes mellitus useful for diagnosis of predisposition to diabetes -
                                                                                                                                                 McGrail M,
                                                                                                                                                                                                                                                                                                                                                                                               Human angiotensinogen gene; AGT; insulin-dependent diabetes mellitus; type 1 diabetes; chromosome 1442-43; single nucleotide polymorphism; IDDM; SNP, diagnosis; susceptibility; transgenic animal; drug screeni antidiabetic; gene therapy; 5' region; promoter; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heterozygous Amp deficiency, including prenatal diagnosis (patients defective in Amp are at risk of developing angicedema if treated with angiotensin-converting enzyme inhibitors), also as antisense inhibitors in cases of excessive Amp expression. The product of the invention is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for gene therapy for treating AmP-deficiency conditions. Its fragments are used as primers and probes to identify patients with homozygous an
                                                                                                                                                                                                                  06-JAN-2000; 2000US-0174700
                                                                                                                                                                                                                                   21-MAY-1999;
                                                                                                                                                                                                                                                                  16-MAY-2000; 2000WO-US13327.
                                                                                                                                                                                                                                                                                                    30-NOV-2000
                                                                                                                                                                                                                                                                                                                                   WO200071751-A1
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91627 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes the isolation of a novel human aminopeptidase P (AmP). This protein is used to produce recombinant AmP and can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC91627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 80-109; 201pp; English
                                                                                                                                                                                (MYRI-) MYRIAD GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 acaaccctgatgacct 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiotensinogen
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                                                                                                                                                   Shattuck DM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC The invention relates to the human angiotensinogen (AGT) gene, some CC mutant alleles of which cause a susceptibility to insulin-dependent CC diabetes mellitus (IDDM, type 1 diabetes). The AGT gene is located CC on chromosome 1442-43, a region linked to IDDM. The invention CC discloses genomic sequences comprising exons 1-5 of the human AGT gene (AAC91600-C91604) and a genomic sequence comprising an alternative AGT CC gene exon 1 (AAC91605). The invention also encompasses the specifically claimed human AGT mutant nucleic acid sequences AAC91667-C91684, and the CC mutant angiotensinogen proteins AAB48945-B48949. The invention also relates to detecting mutant AGT alleles or gene products thereof which CC are related to IDDM; determining whether a person has, or is at risk of CC methods of screening for drug candidates which may be useful in the CC methods of screening diabetes are claimed which comprise the CC mutant AGT, which agonises or antagonises or antagonises wild-type or administration of a compound which agonises or antagonises wild-type or administration of a compound which agonises or antagonises wild-type or compound to a compound which agonises or antagonises wild-type or compound to a compound which agonises or antagonises wild-type or compound which agonises an AGT receptor, which compound which agonises an AGT receptor. Which compound which agonises an AGT receptor which compound which agonises an AGT receptor. The compound which agonises are useful for determining if a person has, or is at risk from developing insulin-dependent diabetes. Mutant CC mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant CC mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant CC mellitus. AGT modulators can be used to treat or prevent diabetes. Mutant CC mellitus or fragments thereof are useful for screening compounds which because of the present sequence represents a human AGT intention of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tryptophan 2,3-dioxygenase; TDO2; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; alcohol; tobacco; drug use; Tourette syndrome; attention deficit hyperactivity disorder; ADHD; schizoid/avoidant behaviour; aggression; premenstrual syndrome; violence; hostility; mania; depression; anxiety; sleep problem; autism; osteoporosis; binge eating; craving; inhibition; PCR primer; ss.
                                                                                              (BLUM-)
                                                                 (TEXA
                                                                                                                                                                                             29-APR-1997;
                                                                                                                                                                                                                                                        29-APR-1998;
                                                                                                                                                                                                                                                                                                                  05-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                W09848785-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tryptophan 2,3-dioxygenase oligonucleotide variant.
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                                                          INC KENNETH.
OF HOPE NAT MEDICAL
TEXAS SYSTEM.
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include: substance use disorders; obesity; alcohol, tobacco or other drug use; Tourette syndrome; attention deficit hyperactivity disorder (ADHD); schizoid/avoidant behaviour; aggression; premenstrual syndrome; violence; hostility; mania; depression; anxiety; sleep problems, autism Methods given in the invention can be applied for diagnosis of RDS or e.g. elevated levels of low density lipoprotein (LDD) or cholesterol, longevity, lack of ADHD, osteoporosis. In treatment of obesity, (A) inhibits binge eating and craving. The present sequence represents an oligonucleotide used in an example from the present invention.
                                                                                                                                                                                                                                                                            deficiency syndrome (RDS) behaviour; or (ii) preventing or treating unwanted weight gain. (A) comprises: (a) an agent (I), i.e. amino acid or peptide, or their analogues or derivatives, that inhibits enzymatic destruction of a neuropeptidyl opiate; (b) a neurotransmitter precursor (II) to promote neurotransmitter synthesis, i.e. L-Tyr, L-Phe or L-dopa (dopamine precursors) L-Trp or 5-hydroxytryptophan (serotonin precursors) or L-Glu (or its sait) or L-Gln (gamma-aminobutyric acid precursors); and (c) chromium picolinate or nicotinate to increase the level of Trp. Typical of many behaviours that can be treated with (A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for treating reward deficiency syndrome behaviour, attention deficit disorders or controlling weight - contains inhibitor of opiate peptide destruction, neurotransmitter precipitals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Page 293; 663pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A composition (A) has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     been developed
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RESULT :
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Best Local :
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                                                                                                                                                                                                                                                            neurotransmitter synthesis promoter; tryptophan-concentration enhancing; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; smoking; Tourette's syndrome; schizoid avoidant behaviour; aggression;
                                                                                                                                                                                                                                                                                                               Human; anti-ADD; anti-ADHD; opiate destruction inhibitor;
                                                                                                                                                                                                                                                                                                                                                Human
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(CITY ) CITY OF HOPE NAT MEDICAL CENT. (TEXA ) UNIV TEXAS SYSTEM.
                                                29-APR-1998;
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                                                                                                                17-OCT-2000
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100.0%; Pr
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Best Local 9
                                                                                  (BLUM-)
(CITY )
(TEXA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis of reward deficiency syndrome. Compositions are disclosed which comprise at least one substance that inhibits the enzymatic destruction of a neuropeptidyl opiate, at least one neurotransmitter, a tryptophan concentration enhancing amount of a mineral compound; and at least one substance chosen from Rhodiola extract and huperzine. The compositions are used to treat ADD and ADHD. They are used to treat reward deficiency syndrome (RDS) behaviours including obesity, smoking, Tourette's syndrome, pre-menstrual syndrome or tobacco use. The presence of
  attention
            Composition
                                     WPI; 1998-610008/51
                                                                                                                                                                                                                                                                                            Tourette syndrome; attention deficit hyperactivity disorder; AD schizoid/avoidant behaviour; aggression; premenstrual syndrome;
                                                             Blum
                                                                                                                                                                                      05-NOV-1998
                                                                                                                                                                                                              WO9848785-A2
                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                AAV72819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compositions used to treat attention deficit (hyperactivity) disorder have of neuropeptidyl opiate enzymatic destruction inhibitor, neurotransmitter, mineral compound and Rhodiola extract or huperzine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blum
                                                                                                                                      29-APR-1997;
                                                                                                                                                             29-APR-1998;
                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                           osteoporosis;
                                                                                                                                                                                                                                                                                        violence;
                                                                                                                                                                                                                                                                                                                         Human; tryptophan 2,3-dioxygenase; TDO2; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity; alcohol; tobacco; drug use
                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                Tryptophan
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV72819 standard; DNA; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enkephalin releasers dramatically improves the patient's response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
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15; Conser
                                                            Comings DE,
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 on for treating rev
                                                                                                                                                                                                                                                                                      hostility;
                                                                                                                                                                                                                                                                                                                                                               2,3-dioxygenase oligonucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                  INC KENNETH.
OF HOPE NAT MEDICAL CENT
TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                           binge eating;
                                                                                                                                      97US-0044394
                                                                                                                                                             98WO-US08684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38
                                                                                                                                                                                                                                                                                                            syndrome; RDS; obesity; alcohol; tobacco; drug u attention deficit hyperactivity disorder; ADHD;
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                                                                                                                                                                                                                                                                                     mania;
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reward deficiency ers or controlling
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                                                                                                                                                                                                                                                                         craving; inhibition;
                                                                                                                                                                                                                                                                                     depression; anxiety;
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94;
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                                                                                                                                                                                                                                                                        PCR primer; ss
                                                                                                                                                                                                                                                                                     sleep problem; autism;
                                                                                                                                                                                                                                                                                                                                                               NO:27
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 behaviour contains
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Compositions used WPI; 2000-678662/66.

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treat attention

deficit (hyperactivity) disorder

Blum (CITY) 29-APR-1998;

Χ.

CITY

OF HOPE NAT MEDICAL TEXAS SYSTEM.

980S-0069886 980S-0069886 17-OCT-2000 US6132724-A

29-APR-1998;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deficiency syndrome (RDS) behaviour; or (ii) preventing or treating cumwanted weight gain. (A) comprises: (a) an agent (I), i.e. amino acid cor peptide, or their analogues or derivatives, that inhibits enzymatic celestruction of a neuropeptidyl opiate; (b) a neurotransmitter precursor ((II) to promote neurotransmitter synthesis, i.e. Tyr, L-Phe or L-dopa (dopamine precursors) L-Trp or 5-hydroxytryptophan (serotonin precursors) or L-Glu (or its salt) or L-Gln (gamma-aminobutyric acid precursors); and (c) chromium picolinate or nicotinate to increase the clevel of Trp. Typical of many behaviours that can be treated with (A) include: substance use disorders; obseity; alcohol, tobacco or other crug use; Tourette syndrome; attention deficit hyperactivity disorder (ADHD); schizoid/avoidant behaviour; aggression; premenstrual syndrome; violence; hostility; mania; depression; anxiety; sleep problems, autism. Methods given in the invention can be applied for diagnosis of RDS or e.g. elevated levels of low density lipoprotein (LDL) or cholesterol, inhibits binge eating and craving. The present sequence represents an oligonucleotide used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   post-traumatic stress syndrome; pre-menstrual syndrome; cannabinoid receptor gene; dopamine DRD4 receptor; tryptophan 2,3-dioxygenase; TDO2; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurotransmitter synthesis promoter; tryptophan-concentration enhancing; allelic polygene diagnosis; reward deficiency syndrome; RDS; obesity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 smoking; Tourette's syndrome; schizoid avoidant behaviour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TDO2 gene G to T variant oligomer #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-ADD; anti-ADHD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opiate destruction inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB; Pred. No. 94; 0; Mismatches
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94;
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Best Local :
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AAZ36290-Z36320 represent genes or expressed sequence tags (ESTs) identified by the method of the invention. The sequences were isolated from rat osteoblasts. The specification describes a method for the identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extraction mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identifications are constantly control samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed sequence osteoporosis; bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (QUAR-) QUARK
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treating or (
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density; bone development; ss.
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                                      The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its
                                                                                                                                                                                                                                                     Claim 1; SEQ ID 17330;
                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and diagnostic, forensic, gene therapy and chromosome mapping prodisgnostic,
                                                                                                                                                                                                                                                                                                                                            WPI;
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Matches 15
        The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                               genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
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15-MAY-1998;
21-OCT-1998;
27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                               AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed
                                                                                                                                                                                                                                                                                                       Claim
negative
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5, Drmanac R,
Ltz D, Kita D,
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receptor-negative breast cancer; lung cancer; ss.
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Randazzo F, Ke
Crkvenjakov R,
Garcia V, Jon
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R, Dickson M,
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Lamson G, Le
Stache-Crain
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
                  detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased tissue in a human, to
                                                                                                                                                       polynucleotides can be used as a source of primers and probes, which coupe used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and
                                                                                                                                                                                                                             of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779.
                                                                                                                                                                                                                                                     differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by
                                                                                                                                                                                                                                                                                               The present invention describes a library of human polynucleotides comprising the sequences given in ARZ12532 to ARZ1779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel human genes and their differentially expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crkvenjakov R,
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                                                                                                                                                                                                                                                                                                                                                                                                               Page 1035;
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rcia PD, Garcia V, Giese K,
am A, Kennedy GC, Kita D,
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                                      sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, particularly L-lysine. The present sequence is a nucleic acid described in the exemplification of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                    Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analysing expression profile or pattern of a gene and identifying homologous gene
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03-AUG-2000;
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                                                                                                                                                                                                  The present invention provides a number of nucleotide and protein
                                                                                                                                                                                                                               Claim
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da M, Ozaki A;
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Best Local S
Matches 15
                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antithflammatory; antibacterial; antivital; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 916; 5507pp; English
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RESULT 38
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Best Local S
Matches 15
                      human secreted proteins expressed in prostate, and encode the proteins given in AAY11716 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/chemokinetic activity, haemostatic and
                                                                                                                                                                                                                                                                                                                                                                                New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematop regulating, anti-inflammatory or tumour inhibition activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostat thrombolytic; anti-inflammatory; tumour inhibition; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
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                                                                                                                                                                                                                                                                           to AAX40715 represent 5'
                                                                                                                                                                                                                                                                                                                                   Page 453;
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     activity,
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                                           of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also use in diagnostic, forensic, gene therapy and chromosome mapping procedures They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untrainlated region (TTR)
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                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                     The present sequence is one of 3351 sequences in a library of human complete the polynucleotides. The library is used to detect differentially expressed genes correlated with a cancerous state of a mammalian cell and can detect colon, prostate, breast and lung cancer. The library can be used to produce probes for detection of mRNA and to produce additional copies of the polynucleotides. The probes can be used for chromosome mapping of the polynucleotide and for detection of transcription levels. Ribozymes con antisense oligonucleotides can be generated. The polynucleotides and their gene products are used as generated. The polynucleotides and their gene products are used as genetic or biochemical markers (e.g. in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical compositions to treat the cancers and proliferative disorders such as neoplasia,
                                                                       Matches
                                                                                                Query Match
Best Local :
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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Reinhard C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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R, Drmanac S,
                                                                       Conservative
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Kennedy GC,
, Dickson M,
s LW, Strache
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Pot D, L
Labat I,
ne-Crain B;
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, Lamson G, Drmanac
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nanac R;
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RESULT 41
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                                                                                                           Matches
                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                           Sequence 391 BP; 85 A; 105 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 842; 1046pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon
                                                                                                                                                                                                                                                                                                 dysplasia and hyperplasia.
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02-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
(CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
                                                                                                           15;
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                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprises 3351 human polynucleotide sequences
                                                                                                              Conservative
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99US-0142311
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                                                     70
  91
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Kennedy GC,
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Kennedy GC, Pot D, Lamson
Dickson M, Labat I, Leshk
LW, Strache-Crain B;
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                                                                                                                                     Score 15;
Pred. No.
                                                                                                                                                                                                                                              130 G;
                                                                                                              Mismatches
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mson G, Drmanac R;
Leshkowitiz D;
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Reinhard C, R
Crkenjakov R,
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 06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                 Library of polynucleotides for diagnosing a cancerous state of mammalian cell and detecting cancer, particularly of the colon prostate, comprises 3351 human polynucleotide sequences -
                                                                                                                                                                                          preventive interventions. The polynucleotides, polypeptides and antibodies against them can be used in pharmaceutical composition treat the cancers and proliferative disorders such as neoplasia
                                                                                                                                                                                                                     blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or monitor the efficacy of therapies and
                   AAC01762;
                                   AAC01762 standard;
                                                                                                                                                                 Sequence 412
                                                                                                                                                                                   dysplasia
                                                                                                                                                                                                                                                                                                                                 Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-091805/10
                                                                                                                                                                                                                                                                                                                                                                                                       Kita
                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams
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02-JUL-1999;
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                                                                                                                             Local
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                                                                                           gctgcactgactggt 74
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                                                                                                                     l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic;
cancer; lun
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d C, Randazzo F,
kov R, Drmanac S,
Garcia V, Jones
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                                                                                                                                                                                    and
                                                                                                                     Conservative
                                                                                                                                                                 BP;
(first entry)
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                                                                                                                                                                                  hyperplasia.
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                                                                                                                                                                113 A;
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g cancer; cancer detection; ;
                                    CDNA; 434
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                                                                                                                            12.2%;
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Dickson M,
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Pred. No.
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nedy GC, Pot D, L
ckson M, Labat I,
Strache-Crain B;
                                                                                                                     Mismatches
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                                                                                                                                     Length 412;
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                                                                                                                                                                                                     compositions
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nanac R;
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derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 1760; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                   sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                             present sequence is one of a large number of 5' ESTs derived from As encoding secreted proteins. An ORF has been identified within the uence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-500381/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milne Edwards
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST;
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mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tag (5' EST) for to 5'ESTs and fo
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Sequence 434 BP; 123 Α, 116 C; 124 G; 70 T; 1 other

87 taaggtgatacttat 101 15; Similarity Conservative 12.2%; 100.0%; 0; Score 1 Pred. Mismatches NO. DB 91; 21; 0; Length 434; Indels 0, Gaps 0

TAAGGTGATACTTAT 361

13-MAR-2001 AAF10271 standard; (first entry) cDNA; 556

Fusarium venenatum EST SEQ ID NO: 2794.

metabolic Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recomb condition; ic pathway e engineering; environmental stress; catabolic spore morphogenesis;
pathway engineering; recombination;

Fusarium venenatum

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RRESULT 4
AAC87968
ID AAC87978
XX AAC87
AC AAC8
XX AAC8
XX DT 07-N
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KW CLAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for monitoring differential CC expression of genes in a first filamentous fungal (FF) cell relative to CC expression of the same genes in one or more second filamentous fungal CC cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS CC are used in the methods for monitoring differential expression of genes CC in a first filamentous fungal (FF) cell relative to expression of genes CC in a first filamentous fungal (FF) cell relative to expression of the CC same genes in one or more second filamentous fungal cells. Monitoring CC the global expression of genes from FF cells allows the production CC potential of the microorganisms to be improved. New genes may be CC discovered, possible functions of unknown open reading frames can be CC identified and gene copy number variation and stability can be CC identified and gene copy number variation and stability can be CC monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore CC engineering. Using ESTs provides several advantages over genomic or CC engineering. Using ESTs provides several advantages over genomic or CC array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate CC analysis of the results. AAF11248 to AAF11853 represents ESTs from Aspergillus oryzae; and CC AAF1879 to AAF13878 represents ESTs from Aspergillus oryzae; and cally claimed in the present invention.
CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory; cadherin-like asymmetry protein; autoimmune disease; immunosuppressive; immunomodulatory; antiinflammatory; antiarthritic; cytostatic; hypotensive; antirheumatic; antianaemic; haemostatic; neuroprotective;
                                                                                                     Human CLASP-2
                                                                                                                                          07-MAR-2001
                                                                                                                                                                                AAC87998;
                                                                                                                                                                                                                     AAC87998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 556 BP; 160 A; 128 C; 138 G; 128 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 86; Page 1396; 3161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                substrate of expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monitoring differential expression of genes in filamentous fungal courses fluorescence-labeled nucleic acids isolated from the cells and
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                                                                                                                                       (first entry)
                                                                                                   genomic DNA from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the present invention.
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Pred. No.
                                                                                                   BAC ref 13.1.
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used to inhibit an immune response in a subject by interfering with th ability of a CLASP-2 protein to bind to another T cell or B cell. An immune response in a subject may also be inhibited by administering an antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides, proteins and antibodies can be used to prevent or treat a CLASP-2 mediated disease, such as an autoimmune disease caused or exacerbated by increased activity of TH11 cells. They can also be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1999;
14-MAY-1999;
21-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                 hypersensitivities, prevent transplantation rejection responses and augment immune responsiveness in immunodeficiency states, inhibit proliferation and differentiation of cells involved in an inflammatory response e.g. arthritis, inflammatory bowel disease and increase differentiation and proliferation of haematopoietic cells e.g. to treat anaemia, thrombocytopaenia and other blood protein disorders. Disorders treated by disrupting CLASP-2 function include multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory, antiarthritic, cytostatic, hypotensive, antirheumatic, antianaemic, haemostatic and neuroprotective activities. CLASP-2 can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypersensitivity; transplantation rejection response; immunodeficiency; proliferation; differentiation; inflammatory response; arthritis; inflammatory bowel disease; haematopoietic cell; blood protein disorder; anaemia; thrombocytopaenia; multiple sclerosis; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
Sequence
                                                                                          rheumatoid arthritis, endometriosis and pregnancy induced hypertension. The present sequence represents a human CLASP-2 genomic DNA sequence from a bacterial artificial chromosome (BAC), given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes cadherin-like asymmetry protein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated cadherin-like asymmetry protein-2 polynucleotide and polypeptide used to diagnose, treat and prevent autoimmune di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu PS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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14-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory responses
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99US-0134117
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99US-0162498
99US-0170453
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   вP;
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G;
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Query Match Best Local Matches

15;

Conservative

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Mismatches

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Gaps

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Score 15; Pred. No

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21;

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Similarity

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84

gagggctgcactgac gagggctgcactgac

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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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US-09-157-17-111
US-09-157-17-111
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LENGTH: 1278
TYPE: DNA
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Sequence 12, Appl	Sequence 12, Appl	Sequence 21, Appl	Sequence 69, Appl	Sequence 50, Appl	Sequence 50, Appl	Sequence 17, Appl	Sequence 10, Appl	Sequence 133, App	Sequence 133, App	Sequence 3, Appli	Sequence 316, App	Sequence 315, App	Sequence 316, App	Sequence 315, App	Sequence 14, Appl	Sequence 16, Appl	Sequence 101, App

ALIGNMENTS

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OTHER INFORMATION: Anglotensinogen, US-09-050-159-123
                                                                                                                                                                              Sequence 12, Application Patent No. 6132724
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 13.0
Best Local Similarity 100
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: No. 6197505berg, Leif T
APPLICANT: Andersson, Maria K
APPLICANT: Linstrom, Per H
TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
TITLE OF INVENTION: COMPOSITIONS FOR USE THEREOF
FILE REFERENCE: 1248/1D042
CURRENT APPLICATION NUMBER: US/09/050,159A
CURRENT FILING DATE: 1998-03-27
EARLIER FILING DATE: 1998-03-27
EARLIER APPLICATION NUMBER: 60/042,930
EARLIER FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 133
NUMBER OF SEQ TO NOS: 133
SOFTMARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                           APPLICANT: Blum, Kenneth
APPLICANT: Comings, David E.
APPLICANT: Ivy, John L.
TITLE OF INVENTION: ALLELIC POI
TITLE OF INVENTION: DEFICIENCY
                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                522 TGGTAAGTTTCACATG
                                                                                                                                                                                                                                                                                                                                                      71 tggtaagtttcacatg
                                                                                                                                                                                                                         Application US/09069886
  P.O.
Box 4433
                                                                           ALLELIC POLYGENE DIAGNOSIS OF REWARD DEFICIENCY SYNDROME AND TREATMENT
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Pred. No.
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US-09-069-886-27

: Sequence 27, Application US/09069886

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Best Local Similarity
Matches 15; Conserv
                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Hodgins, Daniel S.
REGISTRATION NUMBER: 31,026
REFERENCE/DOCKET NUMBER: BLUM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512,418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/069,886
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REFERENCE/DOCKET NUMBER: BLI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512)418-3000
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                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: IVY, John L.
TITLE OF INVENTION: ALLELIC POLYGENE DIAGNOSIS OF REWARD
TITLE OF INVENTION: DEFICIENCY SYNDROME AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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ZIP: 77210-4433
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STRANDEDNESS: single
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X: (512)474-7577
N FOR SEQ ID NO:
CHARACTERISTICS:
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P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Comings, David E. Ivy, John L.
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                                                           Query Match
Best Local Similarity
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                                                                                                                                               TOPOLOGY: line
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hillman, Je APPLICANT: Lal, Preeti TITLE OF INVENTION: NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
307 TAAGGTGATACTTAT 293
                        87
                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 101 base pairs
TYPE: nucleic acid .
STRANDEDNESS: single
                                                                                                                        CLONE: 1649584
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Herewi
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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15; Conserv
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                                                                                                                                                                                  nucleic acid
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3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                           12.2%;
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Pred. No.
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Pred. No.
                                                 Mismatches
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                                                                                                                                                                                                PCT-US95-09261-1/c
                                                                                                                                                                 Sequence 1, Application PC/TUS9509261 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1099 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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 TITLE OF INVENTION:
                              APPLICANT:
                                             APPLICANT:
                                                                             APPLICANT:
                                                                                          APPLICANT:
                                                                                                         APPLICANT:
                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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LIBRARY: FILL
TONE: 1649584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                              307 TAAGGTGATACTTAT 293
                                                                                                                                                                                                                                                                              87 taaggtgatacttat 101
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/212,167
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                                                                                                      STREET:
CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       415-845-4166
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                                                            COUNTRY: Un:
POSTAL CODE:
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                               TELEFAX:
                                                                                                                                      NAME:
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                              TELEPHONE NO: (512)499-4462
TELEFAX: (512)499-4523
                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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METHODS AND COMPOSITIONS FOR THE EXPRESSION OF A BONE AND PROSTATE DERIVED GROWTH FACTOR
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                                                            United States of America
DE: 78701
                                                                                                      201 West 7th Street
Austin
                                                                                                                                    BOARD OF REGENTS, THE UNIVERSITY OF TEXAS SYSTEM
                                                                                          Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/871,033
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19;
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US-09-157-177-111/c
; Sequence 111, Application US/09157177
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; LOCATION:
PCT-US95-09261-1
                                SEQ ID NO 111
LENGTH: 528
                                                                                                                                                                                                                                                                                              GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                    APPLICANT: Monforte, Joseph A.
APPLICANT: Becker, Christopher H.
TITLE OF INVENTION: DAN TYPING BY MASS SPECTROMETRY WITH
TITLE OF INVENTION: REPEAT MARKERS
FILE REFERENCE: GETT:017/GETR017P
CURRENT APPLICATION NUMBER: 05/09/157,177
CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                                                                                          Patent No. 6090558
                                                                                              EARLIER APPLICATION NUMBER: 60/059,415
EARLIER FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                          APPLICANT: Butler, John M. APPLICANT: Li, Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
                                                                  SOFTWARE: PatentIn Ver.
                                                                                  NUMBER OF SEQ ID NOS: 135
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    3143 AATTTATTCCACACA 3129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,430
REFERENCE/DOCKET NUMBER: UT
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Arnold, W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: SERTICH, GARY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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TTY: Houston
Taxas
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TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                              INFORMATION:
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694..2310
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SYSTEM: PC-DOS/MS-DOS/ASCII
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CONCURRENTLY HEREWITH
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Pred. No.
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US-09-328-111-297
; Sequence 297, Application US/09328111
; Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:

, NAME/KEY: misc_feature

; LOCATION: (1)...(564)

; OTHER INFORMATION: n = A,T,C or G

US-09-328-111-223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 223
LENGTH: 564
TYPE: DNA
                                                                                                                                            GENERAL INFORMATION:
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                                                                      APPLICANT: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ford, Donna M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                         APPLICANT:
                                                                                                     APPLICANT:
                                           APPLICANT:
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mes 14; Conserv
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mes 14; Conservative
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, 6262333
                                        Burgess, Christopher C.
Bushnell, Steven E.
Carroll III, Eddie
Catino, Theodore J.
                                                                                               Steinmann, Kathleen Astle, Jon H.
Derti, Adnan
Ford, Donna M.
Lewis, Marcia E.
                                                                                                                             Endege, Wilson
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100.0%;
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; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                        DB 4;
67;
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67;
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US-09-328-111-297
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EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 297
LENGTH: 574
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08845256 Patent No. 5874244
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Best Local Similarity
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                                                                         TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: NOVEL HUMAN GENES AND TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US) CURRENT APPLICATION NUMBER: US/09/328,111 CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Monahan, John E. APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens FEATURE:
                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0277
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: (1)...(574)
                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/845,256 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM CO
OPERATING SYSTEM:
             STRANDEDNESS:
TOPOLOGY:
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                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                               94304
                       : 750 base pairs
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linear
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               single
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NEW HUMAN NADH DEHYDROGENASE
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IMMEDIATE SOURCE:

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US-08-989-289-2
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   Sequence 2, Application US/08989289 Patent No. 5968747 GENERAL INFORMATION:
                                                                                                                                                                 Matches
                                                                                                                                                                           Query Match
Best Local Similarity
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Best Local S
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                        641 TTGTAAATGTGAGA 654
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Local Similarity 100.0%;
nes 14; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/208,210 FILING DATE: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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NEW HUMAN NADH DEHYDROGENASE
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Pred. No.
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Pred. No.
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67;
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                                                                                                                                                                                                                                                   Sequence 70,
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Best Local Similarity
                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Benton,
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                                                                                                                               APPLICANT: Lee, Ving
APPLICANT: Malouin, Frai
APPLICANT: Martin, Patri
APPLICANT: Schmid, Moll)
APPLICANT: Sun, Dongxu
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LENGTH: 877 base pairs
TYPE: nucleic acid
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TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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APPLICANT: Corley, Neil C.
TITLE OF INVENTION: UBIQUITIN-LIKE CONJUGATING PROTEIN
NUMBER OF SEQUENCES: 3
                                                                        CORRESPONDENCE ADDRESS:
                                                                                        NUMBER OF SEQUENCES:
                                                                                                   TITLE OF INVENTION: STAPHYLOCOCC TARGET GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskett
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LIBRARY: AL...
2501808
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                                          STREET:
                                                          ADDRESSEE:
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                                                                                                                                                                                                                                       6037
Los Angeles
California
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                                                                                                                                                                                                                                                  Application US/08714918
                           Suite 4700
                                                                                                                                          Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                          E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Incyte Pharmaceuticals, Inc 3174 Porter Drive
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                                                                                                                                                                                                          Benton, Bret
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67;
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Length 877; Indels

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Gaps

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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskett
MEDIUM TYPE: storage
COMPUTER: IBM Compatible

Diskette, 1.44 Mb

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                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 70 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 70
SEQUENCE CHARACTERISTICS:
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Best Local 9
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                                                                                                                                                                                                                                      APPLICANT: Sun, Dong:
TITLE OF INVENTION: I
TITLE OF INVENTION: I
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA
                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
FILLING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
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                                                                                                           COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                           CITY: Los Angeles
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14; Conservative
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Martin, Patrick K.
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ER: 222/005
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Pred. No.
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US-09-265-315-70/c
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 70
                    SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/26.
FILING DATE: March 9, 1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,9
APPLICATION NUMBER: 13, 1
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 240
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Ly
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: Septemb
                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             523 GGTATTGTAAATGT 510
                                                                                                                                                                                                                                                                                                    STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                   OPERATING SYSTEM: IBM P.C.
                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/009,102 FILING DATE: December 22, 1995 APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: March
APPLICATION NUMBER:
                 FILING DATE:
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Malouin, Francois
Martin, Patrick K.
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September 13, 1996
JMBER: 60/009,102
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                                08/714,918
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ber 13, 1996
                                                                                                  US/09/265,315
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Pred. No.
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RESULT 16
US-09-266-417-70/c
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Best Local Similarity
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                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                               SOFTWARE: Word Perfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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REFERENCE/DOCKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                 APPLICATION NUMBER: US/09/
FILING DATE: March 9, 1999
                                                                                                                                                                                                            OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 90071-2066
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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 REFERENCE/DOCKET NUMBER:
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5. 6228588
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                                                                                                                                                                                                                                                                                                                                          Los Angeles
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633 West Fifth Street
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Lee, Ving J
Malouin, Francois
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ilarity 100.0%;
Conservative
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JMBER: 60/003,798
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240/248
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Pred. No.
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68;
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US-08-874-186-37/c
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Best Local
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1021 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                           FILING COLL
CLASSIFICATION: 435
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 0
APPLICATION NUMBER: 10-JUAN-1997
THE DATE: 10-JUAN-1997
                                                                                                                                                                                                                                    FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Stephen A.
REGISTRATION NUMBER: 38,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Teng, David H-F.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Perry III, William L.
APPLICANT: Skolnick, Mark H.
                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4848
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                               FEATURE:
                                                           MOLECULE TYPE:
HYPOTHETICAL:
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                                              ANTI-SENSE:
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523 GGTATTGTAAATGT 510
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TELEFAX: (213) 955-0440
TELEX: 67-3510
              NAME/KEY:
                                                                                                           STRANDEDNESS:
                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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5989885
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                                                                                                                                         1620 base pairs
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4 (MKK4) IN HUMAN TUMOR CELL LINES IDEN
SUPPRESSOR IN VARIOUS TYPES OF CANCER
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Pred. No.
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Best Local Similarity
Matches 14; Conserv
                                                       Matches
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                                                                                Query Match
                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                    FEATURE:
                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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NAME: OSMAN, Richard Aron,
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59767/RAO
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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APPLICANT: Holzer, Helmut
TITLE OF INVENTION: NUTRIENT I
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NAME/KEY:
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269 TGTAAATGTGAGAT 256
                                                                                                                                        NAME/KEY:
LOCATION:
           14 tgtgagatgcctta 27
                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/222,289 FILING DATE: 04-APR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                         STRANDEDNESS: double
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TGTGAGATGCCTTA 462
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                                                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                                                       2165 base pairs
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370..1434
                                                      Conservative
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1326..1428
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100.0%;
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100.0%;
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                                                                   Score 14;
Pred. No.
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Pred. No.
                                                      Mismatches
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68;
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                                                                                Length 2165;
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RESULT 20
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5194375-5
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                                                                                                                                                                                                        ;Patent No. 5194375
APPLICANT: PARK, LINDA S.;GOODWIN, RAYMOND G.
TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                               SEQ ID NO:5
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Patent No. 5648240
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Best Local Similarity 100.0%; F
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                       NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      2169 TGTGAGATGCCTTA 2156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/248,021A FILING DATE: 24-MAY-1995 CLASSIFICATION: 424
                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                APPLICATION NUMBER: 421,201 FILING DATE: 13-OCT-1989 APPLICATION NUMBER: 366,910
                                                                                                                                                                                                                                                                                                                                                                    14 tgtgagatgcctta 27
              LENGTH: 2466
                                                                                                                                    APPLICATION NUMBER: US/I
FILING DATE: 21-MAY-1990
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                                               FILING DATE: 15-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Jonsson, Klas
Patti, Joseph M.
Sivashankarappa
Tivatnog FROM S
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Pred. No.
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RESULT 22
US-09-079-587-2/c
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                                                            Sequence 2, Application US/09079587 Patent No. 6130066
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                               GENERAL INFORMATION: APPLICANT: TARTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ORDER OF THE PROPERTY APPLICATION DATA:
 APPLICANT:
APPLICANT:
                                                                                                                                                     1759 ATTTATTCCACACA 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION,
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                   107 atttattccacaca 120
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STATE: NEW YORK
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REFERENCE/DOCKET NUMBER: 454310-2990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/816,155B FILING DATE: 12-MAR-1997
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COX, WILLIAM I.
GETTIG, RUSSELL R.
                                                                                                                                                                                                                                                                                                                                                                                                                 212-588-0500
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                               TARTAGLIA, JAMES
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                                                                                                                                                                                                                                 Pred. No.
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US-08-685-871-1
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                                                                                                     COUNTRY:
                                                                                                                                                 STREET:
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Sequence 1, Application US/08685871 Patent No. 6013499
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Best Local Similarity
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        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                             1759 ATTTATTCCACACA 1746
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TELECOMMUNICATION INFORMATION:
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FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/079,587
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MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                     CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                   20007-5109
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3000 K Street, N.W., Suite 500
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                      RHO TARGET PROTEIN KINASE P160
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Akihiro
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Pred. No.
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US-08-342-930-1
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US-08-685-871-1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4739 har-
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Best Local Similarity
APPLICATION NUMBER: US/08/342,930
FILING DATE: 21-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KONSKI, ANTOINETTE F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: 20344-20975.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 7 FILING DATE: 14-SEP-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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448..4509
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100.0%;
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Pred. No.
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; LENGTH: 8561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-112-450-3
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Best Local S
Matches 14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/112,450 CURRENT FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Abad, Antonio Jose C.
APPLICANT: Choi, Gil
APPLICANT: Calderone, Richard A.
TITLE OF INVENTION: Histidine Kinase Two-component in Candida albicans
FILE REFERENCE: Pf393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-02-11
                                                                                                                                                   APPLICANT:
                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             1667 AGGTATTGTAAATG 1654
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                           CORRESPONDENCE ADDRESS:
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            ADDRESSEE:
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                                         MARTINEZ, HECTOR
PAOLETTI, ENZO
PICUS, STEVEN E.
VENTION: VECTORS HAVING ENHANCED EXPRESSION,
VENTION: METHODS OF MAKING AND USES THEREOF
EQUENCES: 48
                                                                                                                                     GETTIG, RUSSELL R.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                     COX, WILLIAM I.
                                                                                                                                                                TARTAGLIA, JAMES
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205..5337
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FROMMER LAWRENCE & HAUG LLE
5 FIFTH AVENUE
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                         11.4%; Score 14;
100.0%; Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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70;
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COUNTRY:

USA

10151 NEW YORK

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10281 base pairs
LENGTH: 10281 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Patent No.
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REFERENCE/DOCKET NUMBER: 454310-29
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TOPOLOGY: lin
MOLECULE TYPE:
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     PRIOR APPLICATION NUMBER: US 08/816,155
APPLICATION NUMBER: 12-MAR-1997
                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1788 ATTTATTCCACACA 1775
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
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                                                                                                                   CURRENT APPLICATION DATA:
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TTORNEY/AGENT INFORMATION
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                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                          CITY: NEW YORK
                                                                                                                                                                                                                                        COUNTRY:
                                                                   CLASSIFICATION:
                                                                                                                                                                                                                        10151
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6130066
                                                                                                                                                                                                                                                        NEW YORK
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PAOLETTI, ENZO
PINCUS, STEVEN E.
NVENTION: VECTORS HAVING ENHANCED EXPRESSION,
NVENTION: METHODS OF MAKING AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                             COX, WILLIAM I.
GETTIG, RUSSELL R.
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                                                                                                 US/09/079,587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local 9
                                                                                                     TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1788 ATTTATTCCACACA 1775
                                                                                                                                     REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01 FILING DATE: 31-JUL-1996 PRIOR APPLICATION NUMBER: US 01 APPLICATION NUMBER: US 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                       FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DAZ: A NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 atttattccacaca 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                              STRANDEDNESS:
                                                                                                                                                                                          NAME: Granahan, Patricia REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 10281 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TODOLOGY. linear
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02173
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                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Hamilton, Brook, Smith & Reynolds, P.C
Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hawkins, Trevor
                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saxena, Richa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reijo, Renee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/742,185
30-OCT-1996
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DNA (genomic)
                                single
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100.0%; Pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 3; Length 10281; Pred. No. 71;
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US-08-742-185-101

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US-08-427-569-14/c
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                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08427569 Patent No. 6235465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: McElver, John A.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Levin, Joshua Z.
APPLICANT: Levin, Joshua Z.
TITLE OF INVENTION: Herbicide Target Genes and FILE REFERENCE: PB/5-30852A
FULE REFERENCE: PB/5-30852A
CURRENT APPLICATION NUMBER: US/09/503,391
CURRENT FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 30
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                               APPLICANT: Kolberg, Janice A.
APPLICANT: Urdea, Michael S.
TITLE OF INVENTION: HTLV-1 PROBES FOR USE IN SOLUTION
TITLE OF INVENTION: PHASE SANDWICH HYBRIDIZATION ASSAYS
NUMBER OF SEQUENCES: 55
                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ATTCCACACAACA 4
APPLICATION NUMBER:
                                                                                                                                            COUNTRY:
                                                                                                                                                                               CITY: Palo Alto
                                                                                                                                                                                            ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road
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                                                                                                                         94304-1018
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Ashby, Carl
                                                                                                                                                            California
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                                                                                                                                             USA
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US/08/427,569
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Pred. No.
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72;
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                                   #1.25
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RESULT 31
US-08-311-760A-315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 315,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity 100.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ramharack, I
                                                                                                                                                            OPERATING SYSTEM: IBM P.C. I
SOFTWARE: FastSEQ Version 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                           STREET: 633 West STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                               APPLICATION NUMBER: US/08/311,71
FILING DATE: September 23, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. Clotti
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                    FILING DATE:
                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                           COUNTRY: U.S.A. ZIP: 90071
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/9 FILING DATE: 23-DEC-199:
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                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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5599706
                                                                                                                                                                                                                                                                                                                                                        633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinchcomb, Dan '
McSwiggen, James
Newton, Roger S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                            IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                     Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                 OR CONDITIONS RELATED TO LEVELS OF PLASMA LIPOPROTEIN (a) [LP(a)] BY INHIBITING APOLIPOPROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                     392
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                     208/155
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Pred. No.
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                                                                                                                                                                                                                                             1.44 Mb
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; TOPOLOGY: 315
                                                  US-08-311-760A-316
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Best Local
Query Match
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                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 316:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: IBM P.C. DOS
SOSTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,
FILING DATE: September 23, 199
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Stinchcomb, Dan T. APPLICANT: McSwiggen, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 633 web. ...
STREET: Suite 4700
STREET: annaeles
                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 10.6%;
Local Similarity 84.6%;
les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 208/155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Los Angeles
                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
                                                                                                                36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newton, Roger S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ramharack,
                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIBOZYME TREATMENT OF DISEASES OR CONDITIONS RELATED TO LEVELS OF PLASMA LIPOPROFEIN (a) [LP(a)] BY INHIBITING APOLIPOPROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                              IBM P.C. DOS 5.0
10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          392
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                                                                                                                                                                                                                                                    32,327
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Pred. No. 2.3e+02;
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Score 13;

DВ 1;

Length 36;

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RESULT 34
US-08-774-310-316
; Sequence 316, Application US/08774310
; Patent No. 5877022
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US-08-774-310-315
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                                                                                                                                                      Matches
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                                                                                                                                                                  Query Match
Best Local Similarity
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Matches 11; Conserva
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                                                                                                                                                                                                                                                                                                               TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Newton, F
APPLICANT: Ramharack
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/774, FILING DATE: December 23, 1996 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/311,760 FILING DATE: September 23, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                           27 acaaccctgatga 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: sing TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 1.5
RRENT APPLICATION FACT.
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                                                                                            2 ACAACCCUGAUGA 14
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                                                                                                                                                                                                                                                                                36 base pairs
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Suite 4700
                                                                                                                                                                                                                                                                                                                                            (213) 955-0440
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                                                                                                                                                    Conservative
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McSwiggen, James
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                                                                                                                                                    Score 13; DB
Pred. No. 2.3e
2; Mismatches
                                                                                                                                                    2;
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2; Mismatches 0;
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2.3e+02;
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                                                                                                                                                                                 Length 36;
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US-08-207-226A-3/c
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                                                                                                                                                                                               Sequence 3, Application US/08207226A Patent No. 5580970
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                            APPLICANT: Hendricks, David
APPLICANT: Rigby, Susan
APPLICANT: Parodos, Kyriaki
TITLE OF INVENTION: DETECTION OF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 223/229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER.

OPERATING SYSTEM: IBM P.C. DOS SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

1006
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LENGTH: 36 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/774,31
FILING DATE: December 23, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/311,760
FILING DATE: September 23, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
                                                                     CORRESPONDENCE ADDRESS:
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                                 STREET:
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STREET: Suite 4700
                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard REGISTRATION NUMBER: 3
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                                                                                                                                                                                                                                                                                                            2 ACAACCCUGAUGA 14
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               SSSEE: Amoco Corporation
T: 55 Shuman Boulevard, Suite 600
Napperville
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California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
Illinois
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 13;
84.6%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INHIBITING APOLIPOPROTEIN
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                                                                                                          HPV TRANSCRIPTS
                                                                                                                                                                                                                                                                                                                                                                                                      .3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 36;
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US-08-425-684-133/c
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US-08-425-684-133
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APPLICATION NUMBER: 07/622,742
FILING DATE: 05-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Galloway, No. 5580970val B
REFERENCE/DOCKET NUMBER: GTR-890:
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 133, Application US/08425684 Patent No. 5834252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local (
                                                                                                        TELEFAX: (415) 326-24
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                             REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: ONE MARKET PLAZA, STEUART STREET TOWER, 20TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: STEMMER PH.D., WILLEM P.C.
TITLE OF INVENTION: END-COMPLEMENTARY POLYMERASE REACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  STRANDEDNESS:
                                                                                                                                                                                                NAME: DUNN ESQ., TRACY J. REGISTRATION NUMBER: 34,587
                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/425,684 FILING DATE: 18-APR-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 39 base pairs TYPE: nucleic acid
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CLASSIFICATION:
                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                  nucleic acid
EDNESS: double
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                                                                    40 base pairs
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04-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                            326-2422
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                                                                                                                                                                                   16528J-015400US
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RESULT 38
US-09-129-740-10/c
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Sequence 10, Application US/09129740A Patent No. 6067246
                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,684
FILING DATE: 18-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US96/05480
FILING DATE: 18-APR-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.6%;
Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 326-2422 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND AND TOWNSEND AND CREW
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MURPHY, ESQ., MATTHEW B.
REGISTRATION NUMBER: 39,787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: STEMMER PH.D., WILLEM P.C. APPLICANT: LIPSHUTZ, ROBERT J.
                                                                                                                                                111 attccacacaaca 123
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                                                                                                            21 ATTCCACACAACA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/675,502 FILING DATE: 03-JUL-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: TWO EMBARCAL CITY: SAN FRANCISCO
                                                                                                                                                                                 Local Similarity les 13; Conserv
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VENTION: END-COMPLEMENTARY POLYMERASE REACTION
                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                           circular
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Pred. No. 2.3e+02
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                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                 Length 40;
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US-08-821-559A-17/c
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US-08-821-559A-17
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10
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Best Local Similarity
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                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
                                                                                                                                                                ATTORNEY, AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 8648.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA OPTICAL STORAGE FILE REFERENCE: DAVID B. MURCHY - Heller 236/119 CURRENT APPLICATION NUMBER: US/09/129,740A CURRENT FILING DATE: 1998-08-05 EARLIER APPLICATION NUMBER: 08/906,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HELLER, MIC APPLICANT: TU, EUGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 42
TYPE: DNA
                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: XIA, YU
                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                STRANDEDNESS:
                                                                                                                                                 TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 21-MAR-1997
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                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                            single
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                                                                                                                    17:
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. 2.3e+02
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 50
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                             PCT-US95-15327-50
                                                                                                                                                                                                                              RESULT 41
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 280
TELECOMMUNICATION INFORMATION: 312/474-6300
TELEPHONE: 312/474-0448
COMPUTER READABLE FORM:
                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                 111 attccacacaaca 123
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                                                              STREET:
                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                57 ATTCCACACAACA 69
                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gass, David A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                   Chicago
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                              Illinois
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                                                             E: Marshall, O'Too
6300 Sears Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Marshall, O'Toc
6300 Sears Tower,
             United States of America
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                                                                                                                            Biologically Active Fragments of
Thermus Flavus DNA Polymerase
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                                                             O'Toole, Gerstein, Murray & Borun
ower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Toole, Gerstein, Murray & Borun
ower, 233 South Wacker Drive
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Pred. No.
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; Mismatches
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ches 0;
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Best Local Similarity
Matches 13; Conserv
                                                                              TELEFAX: (215) 568-34: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                             SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Ya
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMANISED ANTIBODIES NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIDA R.
REGISTRATION NUMBER: 38, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 attccacacaaca 123
                                                                                                                                                                                                          APPLICATION NUMBER: US/08/
FILING DATE: 25-March-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: One Liberty CITY: Philadelphia
                                TYPE:
                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 ATTCCACACAACA 69
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TELEFAX: 312/474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz ADDRESSEE: No. 6180377ris, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE:
COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                19103
                              nucleic acid
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             single
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35,719
BER: CARP-0047
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ER: 28003/31716
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Pred. No.
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Length 70; Indels

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Gaps

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FILING DATE:

03-JUN-1994

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TYPE: DNA
; ORGANISM: Deinococcus radiophilus
US-09-235-246-21
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US-09-235-246-21/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-253-877C-12/c
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CURRENT APPLICATION NUMBER: US/09/235,246A
CURRENT FILING DATE: 1999-01-22
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12,
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Best Local Similarity 100.0%;
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APPLICANT: Higgins, Lauren S.
APPLICANT: Distriction, Michael A.
APPLICANT: DISTRICTION: Method For Cloning And Producing The Draili Restriction
TITLE OF INVENTION: Endonuclease
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             tent No.
             ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                           NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                            TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor TITLE OF INVENTION: Agents and Intermediates for Their Synthesis NUMBER OF SEQUENCES: 73
                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                   STATE: Wayne
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APPLICATION NUMBER:
                                                                                                                                COUNTRY: U.S.A.
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                                                                                                                                             New Jersey
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                                                                                                                                                                              One Cyanamid Plaza
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Hallett, William
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US/08/253,877C
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RESULT 45
US-08-452-164A-12/c
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SEQUENCE CHARACTERISTICS:
LENGTH: 96 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12,
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Best Local Similarity
                                                                          TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 201-683-2158
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: BAIDHARD, ELIZABETH M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368-04
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                       STREET: CITY: Parsippany
CITY: New Jersey
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Conjugates of methyltation: Title OF INVENTION: Agents and Intermediates for Their Synthesis of SEOUENCES: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
 TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 26-MAN CLASSIFICATION: 530
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                              STRANDEDNESS:
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5877296
                              nucleic acid
EDNESS: single
                                                              96 base pairs
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Weiss, Martin J.
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Hallett, William
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                linear
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DNA (genomic)
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100.08; F1
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Pred. No
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hes 0;
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US-08-452-164A-12

Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 18 agatgccttacaa 30
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Db 78 AGATGCCTTACAA 66

Search completed: March 19, 2002, 11:04:27

Job time: 3856 sec
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

TITLE	AUTHORS	REFERENCE	JOURNAL		AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	ATT22F8/c	RESULT 1
Direct Submission	EU Arabidopsis sequencing, project.	2 (bases 1 to 89035)	Unpublished	Mewes, H.W., Mayer, K.F.X. and Schueller, C.	Bevan, M., Zimmermann, W., Grueneisen, A., Wambutt, R., Bancroft, I.,	1 (bases 1 to 89035)	Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	(Arabidopsis thaliana	thale cress.		AL050351.1 GI:4914422	AL050351	project).	Arabidopsis thaliana DNA chromosome 4, BAC clone T22F8 (ESSA	ATT22F8 89035 bp DNA PLN 27-MAY-1999		

	gene CDS	exon gene		gene gene CDS	misc_f	JOURNAL COMMENT FEATURES
/gene="12F8.20" /gene="12F8.20" /gene="12F8.20" /note="similarity to Mono-phosphatase, Streptomyces anulatus, x92429 Contains Inositol monophosphatase family signatures [WVLDPIDGTKSFIT][VLDPIDGTKSFIT]" /codon_start=1 /product="Inositol monophosphatase-like protein" /product="Inositol monophosphatase-like protein" /protein_id="CaB43627.1" /db_xref="GI:4914424" /translation="MASMSKRPNISNESPSELSDTELDRFAAVGNALADASGEVIRKY /FRKKFDIVDKDDMSPVTIADQMAEEAMVSIIFQNLPSHAIYGEEKGWRCKEESADYW VLDPIDGTKSFITGKPVFGTLIALLYKGKPILGLIDQPILKERWIGMNGRRTKLNGED	/gene="T2F8.20" /gene="T2F8.20" /gene="T2F8.20" /number=1 /number=	AMOWK ROULER LIDHLAGT INVESMKE PEAKEKCLED GOVERTIMGUVLWILETA LOLQEAR TOGGE ABETENAK PUVTPGSVPVSDPSPITPSVTTNEAATVPVPAKVEENS GTAVDEHSGTAMFTQFANLNGR" complement (\$1757811) /gene="T22F8.10" /number=1 827010413 /gene="T22F8.20" ROUND ROUND ROUND COMPLEMENT (\$2708340)	/note="similarity to receptor-like protein kinase, Catharanthus roseus, 273295" /codon_start-1 /codon_start-1 /product="putative receptor-like protein kinase" /product="putative receptor-like protein kinase" /protein_id="cAB43626.1" /db_xref="g1:4914433" /db_xref="g1:491433" /db_xref="g1:4914433" /db_xref="g1:491433" /db_xref="g1:491433" /db_xref="g1:4914433" /db_xref="g1:491433" /db_xref="g1:491433" /db_xref="g1:4914433" /db_xref="g1:491433" /db_xref="g1:491433" /db_xref="g1:4914433" /db_xref="g1:491433" /db_xref	ysis .7811	eature	Submitted (27-MAR-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
exon exon gene gene	exon	gene gene CDS	exon intron exon intron exon intron exon	intron exon intron	intron exon	intron exon intron
Complement(126711536) /number=1 /number=1 /number=2 /number=2 /number=2 /number=1 /	/POURCE PROCESS /POURCE PROCES	complement(Join(108/511060,1126/11536)) /gene="T2278.30" 1087511536 /gene="T2278.30" complement(Join(1087511060,1126711536)) /gene="T2278.30" /gene="T2278.30" /note="similarity to dehydrin, Glycine max, AF004807" /codon_start=1 /crodon_start=1	9) 9) 1166 1166 1166 1166 1166 1166 1166	/number=4 complement(91269295) /number=4 complement(92969420) /gene="T22F8.20" /number=5 complement(94219593)	2F8.20" t(8791 t(9059 2F8.20"	ISTRSCPKLSQAYLYTTSPHLFSBEAEKAYSRVRDKYKVPLYGCDCYAYALLASGFVD LVIESGLKPYDFLALVPVIBGAGGTITDWTGKRFLWEASSSAVATSFNVVAAGDSDIH QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QQALESLEWH" QALESLEWH" Q

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                                                                                        Bevan, M., Murphy, G., Ridley, P., Mayer, K.F.X. and Schueller, C. Unpublished 2 (bases 1 to 100469)
                                                                                                                                                                                                                                                                                            project).
AL035679
                                                      EU Arabidopsis sequencing, project. Direct Submission
                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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16990...17148.77278...17407,17493...1
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/gene="T22F8.50"
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VAGEETSLSWLSDGISRNDGSEIKFESAFVSSEGSPLDSFPTSPLSSQSYLHPASSSTL
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/gene="T22F8.40"
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MSSSRSNKALSYDNYINDCFGLQADK. DHHGNRMSKHQQHTCGACSRPLSEKSLMSSQ
KIFWTNELSYSAILACGHVYHGECLEOMTPELDKFDPSCPLOTMGEKKTRAKLSEKALK
VEMDLKARHNKRLRNRYLDSDFDCDDFVMFDHSHRTAAAASKSPRLVSSSSAKSYSAK
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Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich E-mail: michael.bevan@bbsrc.ac.uk
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosome viewed at: http://websyr.mips.blochem.mpg.de/proj/thal/.
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                                                                                                                                                                         /gene="F19H22.20"

join(23475. 23550,24243...)

join(23475. 23550,24243...)

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/note="one AA difference to

contains EST gb:T45164, R90
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complement(20670.
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YKWGNGGWQSSCCTTTLSEYPLPQMPNKRHSRVGGRKMSGSVFSRLLSRLADLTIRIK
SRMKDEVRLVIVFTVDSSVKRQISSSTVLTWFCCFIFATFFSGIAFAFEWTLNGKNHS
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KETKDNNCESLAIVVNSADQKKCMEKIFENKTAKLKRTVSFPLHSQVRSCRTR"
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for analysis and annotation"
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/gene-"F19H22.30"

/note-"ESTS GB.227052, Z29899, H76778, T7634 are in 3' untranslated region
EST 742894 covers intron in 5' untranslated region
strong similarity to ubiquitin fusion-degradation protein
- Mus musculus, Pib:9165348
contains EST gb:AA395284, T42894"
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IVEAKPSNGISIIETDCEVDEAPPLDYKEPERPVAPAPAKGEAKKEVDVAEAEPKFN
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589. .26710,26793. .26923,27038. .27258,27334. .27572,
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AL161594.2 0
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Murphy,G., Ridley,P., Hudson,S., Mewes,H.W.,
Mayer,K.F.X.
                                                                                          Unpublished 3 (bases )
                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1. (bases 1133 to 1779)
     E
                                     Unpublished
                                                                                                                             Zimmermann,W., Grueneisen,A., Wambutt,R., Kalicki,J.,
Smith,A., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                   Robben,J., Braeken,M., Grymonprez,B., Volckaert,G.,
Lemcke,K. and Mayer,K.F.X.
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PNMPKAVAFPVTELIDRKIYVIGGSDTLSPMKSPSRIMMVYDTDTEMMQLRARPDWEA
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27666..2
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28993. .:
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28993. .30105
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/note="similarity to more than 30 predicted proteins,
                                                                                                                                                                                                                                                                                                                                                                                                198987 bp DNA PLN 16-MAR-20
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0; Mismatches 16;
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16-MAR-2000 ment No. 90

Mewes, H.W

Wohldmann, P.,

exon	intron	exon	intron	exon	intron	exon	intron	exon	intron		exon										CDS	gene		gene		source	FEATURES		COMMENT			TITLE JOURNAL	
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intron	qene	exon								CDS	gene	exon	intron	•	exon	intron	exon		intron	exon	intron	exon	intron	exon	intron		exon	intron	exon	intron	exon	intron	
	/number=1 /number=1 complement(join(1116312361,1245512602))		PPPKIVIPPPKIEHPPPVPVYKPPPKIEHPPIVIPPIVKKPCPPKYCPOKYVPVYKPPVVVKKPPVVVKPPVVKKPPVVVKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVKKPPVVKKPPVVKKPPVVKKPPVVKKPPVKKPPVKKPPVVKKPPVKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKKPPVKTPVKT	SAMGODINA A DENTA KANDA SAMON	/db_xret="01:7270860" /translation="MRILPEPRGSVPCLLLLVSVLLSATLSLARVVEVVGYAESKIKT phasegravatackukghevrekgsgatankgreggratornogarreggaar	/product="extensin-like protein" /protein_id="CAB80540.1"	H2/04	97 96646, Z25647, T42523, AIS	roline-rich pro	/gene="AT4g3b//0" complement(join(1116312361,1245512602))	1163. 12602	complement(97299755) /gene="AT4g38760"			complement (95819688)	complement(95399580)	complement(94849538) /gene="AT4g38760" /number=13		/yeire arayooyoo /number=12 complement(9123,9483)	/number=11 complement(90029122) /done="ark4038760"	complement(88299001)	complement(86938828) /gene="AT4938760"	/number=10 /number=10	complement(81628319) /gene="AT4g38760"		/gene="AT4g38760" /number=9	/number=8 complement(78518019)	/number=8 complement(77697850)	complement(76707768) complement(76707768) /gene="AT4g38760"	/number=7 /number=7 /number=7	complement(74177494) /gene="AT4g38760"		

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JOURNAL REFERENCE
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VERSION
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Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                           Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail lemcke@mips.biochem.mpg.de.mayer@mjps.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridguaboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                               2 (bases 1 to 103270)
EU Arabidopsis sequencing, project.
Direct Submission
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                                                                                                                                                                                                                                                              and Mayer, K.F.X.
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Bevan, M., Wedler, H., W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="strong similarity
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Pred. No. 3e-08;
0; Mismatches 16;
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KALEKRONDTAIAFSCAEDVALIEVAHLTGRPYRVESLDTGRLHVETYRLFDTVEKHY
KALEKRONDTAIAFSCAEDVALIEVAHLTGRPYRVESLDTGRLHVETYRLFDTVEKHY
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/gene="AT4g22000"
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/gene="AT4g21990"
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/number=2
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/gene="AT4g21990"
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GTASVADIFNSENVVNLSRQGIENLMKLENRKEAWIVVLYAPWCPFCQAMEASFDELA
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/gene="AT4g21990"
                                                                                                                     contains EST
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esculentum, PATX:E312172
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                                                                     EU Arabidopsis sequencing, project.

Direct Submission
Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-ma
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                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana DNA chromosome AL161556
              lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridg
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
                                                                                                                                                                     Wedler, H., I
                                                                                                                                                                                                                                                     Mayer,K.F
                                                                                                                                                                                                                                                                       2 (bases 167197 to 196247)
Murphy,G., Ridley,P., Hudson,S., Mewes,H.W.,
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                                                                                                                                                                                                                                                                                                                                                       Robben, J.,
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1 (bases 157343 to 167411)
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Arabidopsis thaliana
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E-mail: michael.bevan@bbsrc.ac.uk
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GSIPTSPSGGNGGYLQSSYMAANFREFIEVVFQNWENSVQSWHVSGYSFFVVGMDGGQ
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VATSLNFRIQGHTMKLVEVEGSHTVQNIYTSLDIHLGQSYSVLVTANQAPQDYYIVIS
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QGILINGQFPGPHIDAITNDNIIISVFNYLKEPFLISWNGVQQRKNSWQDGVVGTTCP
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=] dr. 1990/14/ 20/1999/ 2019/07/	/note="Strong similarity to CGI-131 protein, Homo sapiens, AF151889 AF15189 AF15180 AF15180 AF15180 AF15180 AF15180 AF15180 AF15180 AF15180 AF	in(1251712675,1283412990,13090.	/	complement(1251712675) /gene="AT4g21830"		/number=15	11736	: Z	/number=14 1162511735	11469 11624 /gene="AT4921620"	۲,	1142611468	/gene="AT4g21820" /number=13	/number=12 1116111425	T49	/number=12 11095 11160	1087211094 /gene="AT4g21820"	T I	9983 10871	/gene="AT4g21820" /number=11	97029982	D II	/number=10 96219701	-"AT4	/number=9 9426. 9620	92259425 /gene="AT4g21820"	er=9	9087. 9224 9087. 9224 /gene="Art4g21820"	/gene="AT4g21820" /nimher=8	/number=8 88809086	/gene="AT4g21820"	er=7	86438698 /gene="AT4g21820"	0 1	/number=6 85448642	833/8543 /gene="AT4g21820"	ber=6	/munuer=5 /managa1820*	/gene="AT4g21820"

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        Agrobiological Resources, Rice Genome Research Program; Kannondai Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2; Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is a variable and the accession number will be preserved.
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PROGRESS ***, in ordered nia
Aphnozes
                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                            Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                            Published Only in DataBase (2001) In press: 2 (bases 1 to 119807)
                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza.
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Spermatophyta; Magnoliophyta; Liliopsida;
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complement(15183.
/gene="AT4g21840"
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/protein_id="CAB79138.1"
/protein_id="CAB79138.1"
/db_xref="G1:7259028"
/translation="MTAAAVPATGSFQKQDEEWRAVLSPEQFRVLRLKGTDKRGKGEF
TKKFEEGTYSCAGCGTALYKSTTKFDSSCGWPAFFDALPGAIKQTPEAGGRRMEITCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(15183. .15341,15764. .15920,16015.
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/gene="AT4g21840"
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/gene="AT4g21830"
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/gene="AT4g21830"
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Complement(12676. .12833)
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Submitted (13-JUN-2000) Horticultural Science, North Carolina State University, 23e Kilgore Hall, Raleigh, NC 27695-7609, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF277453 162 bp mRNA PLN 05-ÖCT-2000 Arabliopsis thaliana putative PHD finger transcription factor (SHL1) mRNA, complete cds.
AF277453
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Clouse, S.D. and Oh, M.-H.
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                                          VEAIETDARGSHAKVRVRWYYRPEESIGGRRQFHGAKEVFLSDHFDFQSADTIEGKCK
VHSFSSYTKLDSVGNDDFFCRFEYNSTTGAFDPDRVTVFCKCEMPYNPDDLMVQCEEC
SEWFHPSCIGTTIEEAKKPDNFYCEECSPQQQNLHNSNSTSNNRDAKVNGKRSLEVTK
                                                                                                         /codon_start=1
/codon_start=1
/product="putative PHD finger transcription factor"
/protein_id="AAG21353.1"
/db_xref="G1:10644645"
/translation="MPKQKAPRKQLKSYKLKHINKSIQEGDAVLMRSSEPGKPSYVAR
                       SKNKHTKRPG
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/db_xref="taxon:3702"
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/chromosome="7"
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                                                                                                                                                                                                                          /gene="SHL1"
                                                                                                                                                                                                                                                                       /gene="SHL1"
                                                                                                                                                                                                                                                                                                                   /note="similar to BAC clone F19H22 in GenBank Accession
Number AL035679"
                                                                                                                                                                                                                                                                                                                                                                  /chromosome="IV"
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23815 c 24131 g
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  207 c
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                                                     cactgactggt 74
                                                                                       GTTTTGCAAGTGTGAGATGCCATACAACCCTGACGATCTTATGATCCAGTGTGAGGAATG
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H.vulgare (Dbg576)
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1 (bases 1 to 1058)
Speulman, E. and Salamini, F.
A barley CDNA clone with homology to the DNA-binding domain of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-FEB-1994) E. Speulman, Max-Pla
Zuechtungsforschung, Carl-von-Linne Weg 10,
Location/Qualifiers
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Plant Sci. 106, 91-98 (1995)
2 (bases 1 to 1058)
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ES43 gene.
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/db_xref="G1:1345528"
/db_xref="G1:1345528"
/db_xref="SPTREME:Q43479"
/db_xref="SPTREME:Q43479"
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/cultivar="Dbg576"
/db_xref="taxon:4513"
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                                                                                                                                                                                                                                                                                                                                                      'gene="ES43"
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tches 15;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachėophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nemoto,Y.

Direct Submission
Submitted (21-FEB-1998) to the DDBJ/EMBL/GenBank databases. Yasue
Nemoto, Yokohama City University, Kihara Institute for Biological
Research; Maioka, Totsuka, Yokohama 244-0813, Japan
                                                                                            AX059527.1
                                                                                                                                        AX059527
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Triticum aestivum WESR4
AB011445
                                                             thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (E-mail:nemoto@yokohama-cu.ac.jp,
Fax:81-45-820-1901)
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260 from Patent WO0055325
                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="zinc-finger motif"
/protein_id="BAA82157.1"
/db_xref="GI:5360897"
/tanslation="PYNPDDLMVQCEGCKDWFHPTCMGMTIEQAKKLDTFLCADCAKE
NGAKRPSNSYPSSPSSDSKVEPKRKW"
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/strain="Chinese Spring"
/db_xref="taxon:4565"
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/note="salt-stress responding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana BAC AF076274
                                                                        This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problem such as compressions and repeats; all regions were covered by sequence from more than one subclone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
                                                                                                                                                                                                       NOTICE: This sequence may not be the entire insert of this clone It may be shorter because we only sequence overlapping sections once, or longer to because we provide a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 80446)
Edwards, J., Wollam, C. and Dubbelde
The sequence of A. thaliana T27D20
Unpublished (1998)
                                                                                                                                                                                                                                                                                                          MAPPING: Clones were assigned to the YAC map by hybridization by M. Lodhi, Cold Spring Harbor Laboratories, and fingerprinted by M. Marra, WashU, to pick the best candidates for sequencing.
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                                                                                                                                                                                           neighboring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (03-AUG-1998) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis,
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Preuss,D., Copenhaver,G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
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a 8296 c
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/db_xref="taxon:3702"
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                      NEIGHBORING COSMID INFORMATION:
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78.8%;
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C T27D20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missouri 63108, USA
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                                      CDS
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                                    /gene="T27D20.4"
join(22634. .227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="T27D20.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /map="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:3702"
/clone="T27D20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar="Columbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                      22705,22988. .23235,24132.
```

The 3' clone is T24H24, 200 bp overlap. Actual start of this cosmid is at base position 1 of T27D20; actual end is at 80252 of

Coding sequences below are predicted from computer analysis, using the program Genefinder (P. Green and L. Hillier, ms in preparation).

IASNSVFHERTKHIEVDCHKVREQVQLGVILPHYTESEEQLVDVFTKGASTKVCEYIH complement(join(12394. .12788,13045. .13861))
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(Pfam: rvt.hmm, score: 12.22)" /organism="Arabidopsis thaliana" /cultivar="Columbia"

14338...18209 /gene="T27D20.5" /gene="T27D20.5" /gene="T27D20.5" 15011(14338...14992,14834...14890,14914...15492,15554...1. 16094...16517,16614...17066,17127...17229,17278...17578, 17636...17983,18077...18209)

/note="contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35)"

IKLNTHGGLIRMLKNVRYVPNLRRNLISTGTLHSLGYKHEGGEGKLRFYKNGKTALCG
YLMNGLYILDGHTVATETCNAESAKNSTKLLIEKEEFROLDFCEHYVKGKSKKLSFNV
GKHVTEDILGYVHADLMGSPNUTPSIJGKQYELSIIDDKSRKWHLMFLKSKDETFDKF
CEWKEIYENHVGKKVKTLRTDNGLEFCNNRFNDYCAKTGIERHRTCTYTPQQNGVTKR
MRRTTKEKVRSPASAVDHNVPEQLMLKREPGYKHLRRFSJAYVHQEGKLKRRVLKG
VFLGYPQGTKGYKVMLIDEEKCVJISRNVVFNDDSVFKDLGGGSKDEDETVTQESQIEI
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BDKDMEKWHGGMIEBMDSLLKNATWDIVDKFKNGKYLSCHMLYKKLGIPGVELFRYK
ARLVARGFSHREGIDYGEVFSPVVKHTSIRILLSLMVKEDMELEQMDVKTAFLHGELD
OTLFMEQDEGFEAPRQNNKRFNAFMNDQKFSRSVSDSCVYVKEVSNAKSMTEIKKLKX
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.24348,24458. .24691

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ENLGRTYADRRKKFGPINTWGDMKYLLRLRMLSQGTRTVDEYFEEFEKLMNALELEE
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complement(join(27921. .28322,28562.
/gene="727D20.8"
/note="contains similarity to DNA
(cytosine-5-)-methyltransferases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="T27D20.19"
join(40097. .40331,40377. .40461,40515. .40592,40638. .41244)
/gene="T27D20.19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESYKQNEEENARMYDRANSYLSRMRAAEAKVQTLEISNTDLSAKLESGKNAYPTTIEN
ENRSRAELLACEERMKKLEEGGSVMLHAARQEEKRKVRAQLTDPSSKYGTFYVQSDEV
EAANIRAAEVKVNRELLEEIEKGEIPSIAEELESVRADEIKFAQKAAEPKTPRPNPVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MASSSYCAEKKMERERARKEKERLQSDKVVMAGTLEDSKLRALD
KAKQPQNEDDSGTRQKSSALSGKGPKLISTSEARTSKINTPDKEPTKRDADKRKHSET
DARSPSRSSRAGNEAKETGQNQOKGKNIKGBSODLVVLSSRVSESRYSGGRATTSPLDA
PPMPFADTLRTLVHPRAIMPPLAELKATNREKLGEAVQEENYAFLSHEDQLFEKDKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MAKTRPGVAFSSKIKLGKKDIKILGREILLGNVIVEVGFFTVGD
CVLMRPSDAGKAPYVARVEKIEADARNNVKVHCRWYYCPEESHGGRRQLHGAKELFLS
DHEDVQSAHTIEGKCIVHTFKNYTRLENVGVEDYYCIFDYKAATGAFTPDRVAV"
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VETLMMKGIVSQAKKSGEQPPWIRDTLMKQMMVHWNTEDAQLKSETTSNCRNSDRGGL
GVHKHLAGQKSFVQVHQEMERLKRHVSYGEVFMQTHTRVDGSFVDQKSQHVGEAYVKI
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                                                                                                                                                                                                                                                         /note="contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHMARECLNQRVMILTPSGDYESQDEQEDSDEHEDIEYPDVGELLVIRRTLSVFVNLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WNASNNRAMDKSKVVESDHRFKNKSNEAPKTSRPKLGKFPSTNQSRSRYITCFKCQGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="T27D20.3"
                                                                                                                                                                                                                                      codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                             |oin(41442. .41817,41934. .42505)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGTACTACAAATGTGAAATGCCGTATAACTCAGATGAACTGATGGTGCAAT 27787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/this fragment has an overlap with ATCHRIV10 at the 5' end and an overlap with ATCHRIV12 at the 3' end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory, John Innes Centre, Colney Lane, E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamar, B., Stoneking, T., Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II, Brassicales; Brassicaceae; Arabidopsis.

1 (bases 197052 to 198022)
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AL161499
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Lemcke,K. and Mayer,K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
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                    /product="hypothetical protein"
/protein_id="CAB77865.1"
/db_xref="GI:7267153"
                                                                                                           similarity to"
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                                                                                                                                                                                                                                                                8288. .12735
/gene="AT4g03970"
join(8288. .8638,
                                                                                                                                (GB:X56794)
                                                                                                                                                                           /gene="AT4g03970"
                                                                                                                                                                                           jóin(8288. .8638,8738. .8949,8993. .9236,9341. .9454,
9527. .9676,10448. .10561,10690. .10770,10833. .10905,
10956. .11074,11199. .11279,11426. .11509,11626. .11679,
11793. .11986,12069. .12153,12238. .12735)
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(46940. .48645,48865. .49459))
translation="MLADLDKFLSFPWGRESFLKTAVGMRPDKRNLGKSTGKRQLTTD/
                                                                                    /codon_start=1
                                                                                                                                                    'note="contains similarity to
                                                                                                                                                                                                                                                                                                                                     /number=1
                                                                                                                                                                                                                                                                                                                                                         /gene="AT4g03970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/variety="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 to 28786; 28587 to 117434; 117235 to 197680) Stoneking, T., Stumpf, J., Mewes, H.W., Lemcke, K.
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78.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34.4; DB Pred. No. 0.32;
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Σ.	/number=10 1142611509	1128011425 /gene="AT4903970"	/gcue- arygosio /number=10	11199 . 11279 //eene "ATA/013070"	T = 7	/number≖9 1107511198	1095611074 /gene="AT4g03970"	/number = 8	10906. 10955	/gene="Ar4g03970" /number=8	1083310905	- T	/number=/ 1077110832	ν.	/number=6	/gene="AT4g03970"	/number=6	1044810561 /gene="AT4q03970"	/number=5	967710447 /gene="AT4g03970"	/number=5	9527 9676 //gene	/gene= A149039/0 /number=4	94559526 /respective/13970"	/gene= 814903970 /number=4	9341. 9454	/gene="A14gU39/0" /pumber=3	92379340	/gene="AI4gU39/U" /number=3	89939236	/gene="AT4g03970" /number=2	89508992	1	8738 8949	/gene="AT4g03970"	Ϋ́	NHLQGALASS AAAAMASKYAWSEEMAQE I VGENTEWEADIUT I I LEMIMUSAHWYGLA INLGVWSVEILDPNTDLYEEDEVRRF I EPVYTIMPYLIQRYCKPECSQNHGLQPFYWK	EHLTSSGYLISNKFLLSLAKPTNWVSTLHMEVLVSLLSQKLATTLINQRAAFVQPWFA	DDTMKAMVIYSHPIHDTNSKPNKQLESSPTPTEDQITDSQDIGAHDLDENQEEGYVDV SDSSPAREREKPTLSEAEVFLVAELLSKSKTGSYELLPSMSKSEFALFRNTLSAAPNT	LCLSHHIFVYYNIQDTMEAAAASHSLLGFAKFAKKKVTLESAAVSQALSQTPPEVNFD	NPVYDTDVKDQNANEEDVDSQMQDASERVPTTHSGLDLPKEHNSEELETNANETDVDG KMQDSLDRETASHSHTDLPTDQSSEEQOQAKTMSELTMVFKKDVNLMSETNTAAAANNTV	VEGQPEVAQQVPDDHLDKTQDSSDSIPLINTEITDDPMDVFVTPLQSEHSNKDDANEG	KTDWPGGDATLPPISVPKKKQSRGHCGPRRYSTRSKPELNLSDDEKSRLISELQTKVE	PIKSLVSQLQQKTFRLKGFPPALQLIAFRNIPGLLDLVLDDSTSKTILLWKRLTHPKQ VISLPQIHALESNLKLPVDPLIVGDLNADQSWAEWDDEVKDKKVAYMYDLIWVSHQFQ	
Query Match			CDS	gene	gene		exon	11111	5 + + + + + + + + + + + + + + + + + + +	exon		intron			٠									CDS		exon	gene	1	misc feature		exon	TUCTOR		exon		intron		exon		intron		exon		intron	
28.0%; Score 34.4; DB 8; Length 198022;	/codon_start=1		/yene- A14903550 complement(join(3125631513,3171831843,3196432611))	complement(join(3125631513,3171831843,3196432611))	31256 32611 31256	/gene="AT4g03980" /number=3	/number=2 2807428320	/gene="AT4g03980"	/number=2 27956 28073	2705327955 /qene="AT4q03980"	/number=1	2694527052 /appa="ATM/03880"	HPNGUMEXWELPUTVSEVICLPPSTRVPSGRRKKKKIPSVWEHGRSQPKPKLHKCSRC GQSGHNKSTCVAAI"	THLVNLDKRTCTCCMFDIDKFPYAHGIASAKHINLNKNMFVDEFHSTYRWRQAYSESI	NSDKKLAQYLWEVDVRKWSRAYSPSNRYNIMTSNLAESVNALLKQNREYPIVCLFESI DSIMTBWENEDDERSSONDSAVTINVGKKMKASYDTSTRWI EVYCOVNOFFERVKGDTK	KGTLLGASAQUGNENLE SAEALVUTENDASMUMELACULNELEDENDLYE VSURAAS IASGLSENYPLAHHGLCTFHLQKNLETHFRGSSLIPVNYAASRVYTKTEFDSLFWKIT	FRKDHGVGINYSKAWRVQEHVVELARGLPDDSFEVLPRGYKLMRKVISIDGAHLTSKF	ADSLFIGKKFKDKDEMVFTLRMFAVKHSFEFHTVKSDLTRYVLHCIDENCSWRLRATK AGGSESYVIRKYVSHHSCDSSLRNVSHROAFARTLGRLISNHLEGGKLPLGPKOLIEI	/translation="MFKVSFLFWQPRLTSRIIQACVSETSSIFDQQYSSSAFSTGLSD	/protein_id="CAB77866.1" /db_xref="GT:7267154"	/product="putative transposon protein"	mudrA protein (GB:AL021710)"	/gene="A14903900" /note="similarity to similar to maize transposon MuDR	join(2635226944,2705327955,2807428320)	/gene- A14903980 /number-1	26352 2694	/gene="AT4g03980"	· "	/number=15 20580, .22438	- 3	/number=14 1223812735	/gene="AT4g03970"	/number=14	1206912153 /gene="AT4g03970"	3 7	1198712068	11 2	11793 11986	/gene="A14g03970" /number=12	1168011792	ત ક	/number=11 1162611679	- 3	/number=11 1151011625	

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KEYWORDS
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AL161773/c
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                                                                                                                                                                                                                                                                                     The true right end of clone RP11-212E4 is at 154195 in this sequence. The true left end of clone RP11-291I6 is at 133478 this sequence. The true right end of clone RP11-472K17 is at
                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-212E4 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contilys of human chromosome 13 constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt Wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                      in this sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chr13
RP11-212E4 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jul 19, 2001 this sequence version replaced gi:13751315.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 154195)
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                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.chori.org/bacpac/home.htm
                                        /note="L2 repeat: matches 2693.
                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                               Location/Qualifiers
  'note="AluY repeat: matches 2.
                                                                                note="AluSx repeat: matches
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                                                                                                                                         /clone="RP11-212E4"
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21600. .2
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21593. .2
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21589. .21
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                                                                                                                                                                                                                                                                                                                                                                     /note="19 copies 22 mer 61% conserved"
21571. 21990
                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2 repeat: matches 2490. .2708 of
21566. .21983
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                                                                                                                                                                                   /note="11 copies 36
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19821. .19872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="14 copies 33 mer 89% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="5 copies 33 mer 83% conserved"
18676. .19822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"L1ME3A repeat: matches 6034. .6158 of consensus"
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14560. .14837
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50923
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/note="15 copies 2 mer tt
61468. .61770
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/note-"L2 repeat: matches 2592. .2671 of consensus"
51533. .51968
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/note="34_copies 2 mer ca
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44551. .44586
/note="9 copies 4 mer tcat 86% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33894. .33941
/note="24 copies 2 mer at 75% conserved"
36836. .37970
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/evidence=not_experimental
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/note="Alusx repeat: matches 6. .301 of
                                                                                                                                                                                                                                                                                                                                                              note="THE1C
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="AluSg repeat: matches 1. .290 of consensus"
16788. .56865
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19666. .49737
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26684. .26812
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                                                                                                                                                                                                                                                                                                          'note="L2 repeat: matches 2605. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluSq repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="17 copies 4 mer cctt 67% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                           note="HY3 repeat: matches 1. .78 of consensus"
                                                                                                                                                     27.5%;
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9. .40219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Only in DataBase (2000) In press 2 (bases 1 to 166266). Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 166266)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 166,266 genomic DNA of 11q22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguencing vector: PCR products; 100% of reads Seguencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 155729 bases at least Q40 Consensus quality: 160730 bases at least Q30 Consensus quality: 162836 bases at least Q20 Insert size: 164766; sum-of-contigs Quality coverage: 5.73x in Q20 bases; sum-of-contigs
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107839
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Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humbraft11
Center clone name: RP11-727G17
                                                                              144192
151056
                            156286
159077
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Center code: RIKEN
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43658 43757: gap of 100 bp
43758 60093: contig of 16336 bp in length
60094 60193: gap of 100 bp
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12407: contig of 6882 bp in length
124147: gap of 100 bp
131440: contig of 7293 bp in length
131540: gap of 100 bp
131828: contig of 7288 bp in length
138928: gap of 100 bp
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144091: contig of 5163 bp
44191: gap of 100 bp
150955: contig of 6764 bp
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166266: contig of 1070
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTTTTAAATTAAACATGTATTGTGTGTCTTATTTTGAAGCTATTCCA 123908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Pollara, V., Roymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., P., Rothman, C., Roymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Roymond, C., Riley, R., Rogov, P., Rothman, D., P., Rothman, C., Roymond, C., Riley, R., Roymond, C., Riley, R., Rogov, P., Rothman, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond, C., Roymond
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W Young,G., Zainoun,J., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                            All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                         Submitted (08-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 10, 2000 this sequence version replaced gi:7331563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l (bases 1 to 185404)
Birren,B., Linton,L.,
                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, 55 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 1, clone RP11-304II1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC025409.3 GI:10047870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 1 clone RP11-304I11 map 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC025409
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Center code: Web site: ht:
                                                                        Center: Whitehead Institute/ MIT Center
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37047 c 36491 g 44059
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159077. .162099
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56.9%;
                                                                                                                   Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                             for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ye, W
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            943: contig of 9433 bp in le
9434 9533: gap of 100 bp
9534 10744: contig of 1211 bp in le
10745 10844: gap of 100 bp
10845 12149: contig of 1305 bp in le
12150 12249: gap of 100 bp
12250 13273: contig of 1024 bp in le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 3.8 in Q20 bases; Quality coverage: 3.3 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Phrap; version 0.960731 Consensus quality: 158038 bases at least Q40 Consensus quality: 173087 bases at least Q30 Consensus quality: 177952 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L8126
Center clone name: 304_I_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soon as it is available and the accession number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 157000; agarose-fp
Insert size: 180004; sum-of-contigs
14 60883; gap of 100 bp in le 16291; contig of 1608 bp in le 12 62591; gap of 100 bp in le 162591; gap of 1417 bp in le 162591; gap of 100 bp in le 16332; contig of 1244 bp in le 16352; contig of 12452; cont
                                                                                                                                                                 100 bp

18 57905: contig of 1388 bp in 16

06 58005: gap of 100 bp

59297: contig of 1292 bp in 1e

18 59397: gap of 100 hn

18 60783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --//9: gap of 102
16942: contig of 1163
17042: gap of 100 bp
18595: contig of 1553
8695: gap of 1553
19867: rrr.
                                                                                                                                                                                                                                                                                                                                                          27953: gap of 100 bp 29293: contig of 1340 bp in length 29393: gap of 100 bp 53904: contig of 24511 bp in length 54004: gap of 100 bp 55149: contig of 1145 bp in length
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93191: contig of 2244 bp in
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TITLE
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SOURCE
ORGANISM
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AUTHORS
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VERSION
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AC027308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                     Consensus quality: 242878 bases at least Q40
Consensus quality: 257347 bases at least Q20
Consensus quality: 260576 bases at least Q20
Estimated insert size: 250000; pulse field gel estimation
Estimated insert size: 250000; pulse field gel estimation
Quality coverage: 4.84 in Q20 bases; pulse field gel estimation.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 32 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Feb 14, 2001 this sequence version replaced gi:9256699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
Center Project Name: 85939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 265815)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center clone name: CIT978SKB_56J15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC027308
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provided by the submittor.

This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.

1 1204: contig of 1204 bp in length
1205 1304: gap of unknown length
1305 37886: contig of 36582 bp in length
37887 37986: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7308 265815 bp DNA HTG sapiens chromosome 5 clone CTB-56J15, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -Genome Center
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13374. .14552
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10845. .12149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:12830156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47;
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WORKING DRAFT SEQUENCE,
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                                                                                                                                                     BASE COUNT
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Best Local S
Matches 61
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         Conservative
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                                                                                                                                                                        /clone="CTB-56J15"
/clone_lib="CalTech human BAC library B"
a 49052 c 51296 g 83162 t 3181 others
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
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                                    25.7%;
55.5%;
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265815: contig
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                                    Score 31.6;
Pred. No. 3
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of unknown length
ig of 5454 bp in length
of unknown length
ig of 5802 bp in length
of unknown length
ig of 1440 bp in length
of unknown length
of unknown length
of unknown length
of of 1461 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of unknown length
g of 9466 bp in length
of unknown length
ig of 4603 bp in length
ig of 4603 bp in length
ig of 8126 bp in length
ig of 8126 bp in length
of unknown length
of unknown length
of of 6611 bp in length
ig of 6873 bp in length
ig of 6873 bp in length
ig of 4447 bp in length
of unknown length
ig of 4447 bp in length
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ig of 4447 bp in length
ig of 4447 bp in length
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g of 5100 bp in 1
f unknown length
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g of 4244 bp in 10
f unknown length
g of 1791 bp in 10
f unknown length
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f unknown length
g of 12481 bp in
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of 1553
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of 1892
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of 11908
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Gallus gallus
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Molecular cloning of a cDNA encoding the glycoprotein of hen
oviduct microsomal signal peptidase
Biochem. J. 282 (Pt 2), 447-452 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (05-UUL-1991) M.O. Lively, Bowman Gray School of Medicof, Wake Forest University, dept of Biochemistry, Medical Center Blvd, Winston-Salem NC 27157, USA
2 (bases 1 to 799)
                                                                                                                                                   Similarity
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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/translation="MMTVLSRANSLFAFSLSVMAALTFGCFITTAFKERSVPVSIAVS
/translation="MMTVLSRANSLFAFSLSVMAALTFGCFITTAFKERSVPVSIAVS
RVTLRNVEDFTGPRERSDLAFVTFGLTADLQSIFDWNVKQLFLYLSABYSTKNUALNQ
VVLWDKIILRGDNPRLFLKDMKSKYFFFDDGNGLKGNRNVTLTLSWNVVPNAGLLPLV
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/cell_type="tubular gland
/clone_lib="lambda gt11"
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/protein_id="CAA43208.1"
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White,O., Hickey,E.K., Peterson,J., Umayam,L.A., Utterback,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 23366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPSSLALVPYSRPLSSETVCFFSKHCGYNALDLIEKVILSATSSIVLKNVVPSSKSLA
QALILKALQGVPVSIHCPHKTLKALGDLSKQTNVTLYSSHASSDKQTLIVDEHQVVTG
ARNFTTTSLHREANLMMRISSLDLANLLEKNQKGEVCLGQQKVCYCPISKNKKGGNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: Chlamydia complement(136. .1230) /gene="TC0435"
                                                                     /product="phospholipase D family protein"
/protein id="AAF39290.1"
/db_xref="GI:7190479"
/translation="MDP1RGEHQKKSSKKIRSFLSFMRINETHLFVLQERFLSWGGGA
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VYSSLFSWIPARRTLLTPSPYQQKEIFTEKVQKLPTPSSLALIPYWNSPSSESICFFS
KHCGHDAINVIETAILSAKTSIFLKIFSISSKKITRALAIKSIQGVSVSMLYHHISTK
                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GB:
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:2444077; identified
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(136.
/gene="TC0435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE002160
TYSDLSKTTIELIQFQENSHALLHNKTLIIDKQQIITGNGNFTSASLCEDVNLMMRIN
NMHLASLMEKNQAGRACIKKQKVRYLPVNRKGEIVKEIQKASSSIQLGMYILTNEAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(1247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DLCTWWRSLCDSSTAITYEEAENADSSSSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EILKEIQKATSSIQLGTSCLTSQSIILALDEAVTRSVIVTVIIDSNNKQYTLEKLSSL
CTKINIRVGTRSSSNCQVCIVDHTTAIIGCSSNRPTRRQNANQEAVLIISPLTECQKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="phospholipase D family protein"
/protein_id="AAF39289.1"
/db_xref="GI:7190478"
                                                                                                                                                                                                                                                                                                             /transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="TC0436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="TC0436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Chlamydia muridarum"
/db_xref="taxon:83560"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muridarum,
                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MVSPLITTTSPYLLTLQARLLFTLTTSCSSQNQKTCAKKIQELT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    muridarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   section 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shen, C., Gill, S.R., Heidelberg, J.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2431)
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                                                                                                                                                                                                                                                                                                                                                                                                                           GB:AE001363; identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
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gene

TVIIGSANWSNRGLNTNKEDLLIISPLTEGQKQDLCTWWHFLCENSTVLAEETKTPKI

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FVLENGTAKFITNRKHIVYSPKPYSELAVTQSRDIKAFVQGNTGCSYVFSTIYRSSQK
TQQTELTLVDDDVYAQTIDVSSILPTLILAKKSGDNQIDFEFSSSHHLMAIRVSWKGV
IPERTAVKINNETILALGWLNAKLMASRNPSYWNLLYYNRNVIPERVEDVKSLNNTVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GNFLLDLRQNPPILKGDRSYNSNWRIGNKAGWTDWQIRDRIGYGYRISPTSALARGHA
NSFWPPELPTIPKGDYRTVILGYGTTYEAVTEVYYLSNKVVWREAVMESSSRYYRPPL
TAKSKLSTI IGGDSPLTYIPVRLIEKDEKENIDHAASYKYLNIKGGKGGLTVQIGG
AGFYNLTGTLAATNTISFRAIPAPGYVENLSLUEQDWPLIRPMGTEEKELKIRQTGF
NTILGSSEGNDTLTGGNDTKFYSSPGGGTIYSGKGKVEYHIPQLTHPLHIILSKGSSA
HQLVTENLADQVKPVLGSLSLISSMELLISKQEHVSSEDTKEDLGYWKERYENLGDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GMSFGVENGVESDHTMISIAPGFFNGASYSMQHYLSALYEIHRHIHLGSLTSDLIKKE
LESKGAGCFVHEERFDSLLKASSEKQYLSLTEIHKSLSNQVHLAEAVSHLMNTALPGV
GKIIEREGDFGRLGITTTETSVAMRSYDYRGIGVSKDLFSLPQEVPTIQNVVEQAKYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRETVLSGEFFKTLDDLKHLNHKALIGGHLVEDFIGKSLFSEFRODTIIĀGALSTLGI
TGPDLTVDEMKTY FRSLGPIGKDY LEGKKLGNKĀFLGSYNKI VE KEGKQTEDWLHPVTV
GANDVTPADESTWCGIKORCLÆLIESDESKFRPETPKGISRTKIDKVTPTKLMSEOS
GANDVTPADESTWCGIKORCLÆLIESDESKFRPETPKGISRTKIDKVTPTKLMSEOS
KRALSPELLDRENELIEĀKNFDLIKFTDVDRALYVLRNQVCDDASĀSAAVFSLQLQLĀ
ELLRGTSFP IANQLNVFPDLNRNIĀSSLEKTIKLY LGSHGQTETV IWHSAISDRVMFL
RDMLATĀBEMĀRLVKESIFKSETPLTTPEEIKLINSWĀELQSKDNLGILGEEVDKLDE
DDMLATĀBEMĀRLVKESIFKSETPTTPEEIKLINSWĀELQSKDNLGILGEEVDKLDG
VTSSIMENSKLKKRVĀAIEDSIVĀGYFYLRLEETISEMVRIPPKDLKKRVIRFMEGMD
                                                                                                                                                                                                                                      KLPLETTLTASYYLXPVSGDLYVTCLMNRRPQNQAFVIRFKGYKFQKGAFRSIALISS
HSVGESRIAKTVLQFRGQELFHLEKSAPNKSAVLQLDSKLLSLSRMLFYGGDQVIRYT
                                                                                                                                                                                                                                                                                                                                                                                         VSDTSLKLENFVRYLMEAET IELYRQLLYAQNLLRIHNRDLVLKLFYVRQSEGMGAVL
ITFKNFFIESMEGISAPTLEREAKPILASDPMGLINPAYREHLDLFLGEDKLNLAILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLETALGAWNLYDSVVSLKEAQTHSDRMAARVDIAFNSITLGITIASVALPSLMLAVG
PLAAIGMGASAIARNVALKEERYDQWLVYKKFLTEGGSHILFADPDRHLLDFSGNYVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKQFSAKANELGATGVMDLELGMSIVSIVQYMRLLEEGKGKDPLAVANLVMDVKETAE
MTVGAVIQGLSKKFITQEGVDGFRLETAIASQLKKASSRVGGSVGKVFSKTAAVLELP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIEDMYQVSPHIKQRYGFSETLSVREOLQVYFLDAPEGIQSLLSFTDAGLLSSHQATT
LEKMRERGPVIIERIQTTWGKLYEIGGSIHHRRIDEFTSETDLDEMKLNGDVLTDFLT
KHVLDSETVSLILVLLETRGLEEGTKHVSRSLIVETPDEAASLFQFLKNKTAKTREML
VSLLSEVTDKLKSAQLDGEDVEVSRVSFSDNSDEITVEVKKGSLLKKLSIRGGGIFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSWPEFYNRYANAWSDLATHYGAEILEAHPQSFLYEVEGRCMGLSLLYMSIEDEGGY
RTLQGNLDTVSALYQQKERDHLPLSSKDQSLLSRDLSLINWLQYQGNKVLLENRGFNH
AKWDVLQLTSTFEKSLTKSLLITTPTHSLTLNFMGSFFRVTDPNFGHVDFPSLAAALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANQQHPDERGGRWYSQLYDESFKKRVTAPVKKIQELAKKYLNEQRVHVLEIDDYLTKN
PLFNRLHEEGYAFSDLTEITRYMLAEYGISGIFSEGNILPSPSARLVNIIKTYYGGDY
HDMQDVLPKIYDWLASGGAADLTNERFAAIPESLRKNLEGLHGTDLLTPPVDASVSGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQOYKOLIKANEQKIKOIVGKVNTDLGKERVFIKNIRDLSSKQDRTNTYNYEMEMLLR
WNYPAASDQIRMYMLKELGGIYTDLDMMPQYSPDVLQMIGGDRFFEELPIRRAVS
DGVLKLALANGESGITIONIAQDIDISKLIRSDRTOLEKLITDIENKOKSGSTSKFESLG
RMAPDSVRDFMPILQRHHKWSTGWNVRGLNGLMMAHKGSAMVDAVIKGQRQAYRELKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFNSHRVKIDSHFHGIWIAGAPPEGTDVYIKTFLQTYEEFDFLFWVDRQAFGAAKFSSILKKLAFDSSLKELRSITSQETQDFVKEYDELQAKYQTSGRREERRELEKDLRKLFDR
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SLKATKSIRRRKPRSVEEKREQLVKDPADKIVYDLRADTIASRLKLTEEQIQKCRISL
                                    RVLKANKNVITIPMKSSYTKK"
                                                                                                                                             PNVINNAITYYRVVVPFWIRNRLTKGSLIRIPAHSIPIALTTTQNDVFKTIYAPGFSI
                                                                                                                                                                                            PLSVQQFLSLDDLWLADLKERVMNANEEGFKLISQMHDSYLMESCMNLRDAVPQWKIN
                                                                                                                                                                                                                                                                                                                                               QEFSMLQYIVSMQEGKALGSLLTPPRYKDMNLAVLTYTVASSWEGRREASWLKAPIEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVPAHKTKYLFFTDEESLANPEDNVLFYSKLGSNTLQASQKPLTQFARQLWASYDEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMPPNTKRNGEHVFA I ENQEGVDVKVLGF LQSGHVLGEY EEDLMY KDVFARK I THFAV
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13043.
                                                                                         YESFLGLDAFLKPRTHNRVGDMLLELEKEVVVTVKKVDETDYNKKRVYIVTELTKEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITATPIDQMNAGTRLVTMGVKTCDVAKWQKQHPTETSYPEDILDWLTQKSWFLAPEVL
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/gene="TC0437"
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/db_xref="GI:7190480"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="adherence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similar to GP:6013469; identified by sequence
. 23050
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VTNHVHEFPQ1IOSLEDSDYVAKIXLELKYSSTTTVUHHSSQQNLSLEFKELLK
RVALVHLLNPEEAAKARKALEKKERDKKGKQOEKDSSEEDQGGOOKKRPSEYABLLK
QYEQHKAKDSLGLLSEAEOMTFLEITTG1TAENPTLFSVISQIEAEISSGYVFRALESQ
VSKWFSLPEQGORQQILMLKELEKDAIKNSKODKKDHKWMLETLYDQAEOKWLOEK
KKLODLIKNGGDNSRVILKDSDQLLSRNELFQSMIKKGYPFADFANILERDVADAGIS
GIFSSKAIFPAPSKQILVLKKTLGGDPATTQDALPTVDWILEEPNSETINKLFKQF
PENLQKELKNIAPEHLLTPPIDTSVSALGMRFSTEVGLESDSVMASIGSGFRNSSYS
MARYMEAIFELQOKIVNGELQTVETVKNILOKKGAESLYHADRAALLVQESELKYHLS
LTEVQKGLADLDNLGQAPSYLLTGPLFGLGHIMLENDEGLFLATSMTDDIGLSTYDF
SGIGGRKDVFSTPSEVPSITTILDRVKYDTFSWFKFYERYSGIWGDLAFRLGAESLRT
HPQTFIYDTEGRCMGLSYLFLAAENIAAYGILQDNLSTLAALFEKSSVFGVLLTFSHAV
TLHFFDGAFRVTDPHGBYDFPSLESALYFLEYMVQISSDVRAQTGKEGVSVPQULX
TLHFFDGAFRVTDPHGBYDFPSLESALYFLEXKVLDEREKYPGVLYTPSHAV
TLHFFDGAFRANNIFTDAGLVFGYQMTFLDRMITVRGARSGGIRTWATLFAMGLTL
NGNRIDERTKESDLDKTQINGDLLTSFLEKKVLDERGVALGRTLVETLFPVGTGLUS
SGAIVETPDVASLLQASRERLSHFKDVLQVLLRELARTKGHGLKDSKVSVXSVTV
EPSGEAAIVLEKQDTPKKTSSYTISKIKISKILERAFGKLLANTGVADVELGLS
EPSGEAAIVLEKQDTPKKTSSYTISKIKISLARTKGRGLKDSDKVSVXSVTV
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LFRSYLEPKTLEVRSGTPIDFHVWSQYDKIHVHATTLKLEKFQVYNVTTATDALNRYL
MYAQNLAYIYGRDFVLKFFFIRSGTGIGAIQLVFKDLFKDSFGTEKTLGKEAKSTTPL
                                                                                                                                                                                                                                                                          SSGGGKIFSGLGKNWYHIPKLKGRLDIILAKNSAEHLLLMDDYSYNWQSLGTNLTLIP,
RGEGNNNSGIFVSNFDASPSFEQWYNKFTYKKAADGITLFAKSEDQNFSLATTNTI
VTLCYHSVDQTIWSNKLPEEPSYIENIFNWLKKFCWWLAPKVTVLQREGTADFYYROG
KLIYHPKPFAELDLHPQPGYHTYVNGSIGDTYIFSESPWVNLSTVKLSLADDLGHSQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSLIQYARLYDAGKGSSPEALFNLILDVKELTEMTVGTVIQALQKQFITPAGIDGFR
TETLLARQIQKVGTRVGGTVGKALGSVARVLELPVLETIAGVWGLVSSVEDLLHADSY
SDRVAAKVQISFDVITLALTLSSALAPLAMLAVGPIAAIGMGAASIARNVARKEERHY
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STWCGSKKRCVAELLFSDSSTKLSTNKLQGVTRTKIDTSTFTSLWKEESKKKLPPGLL
ESFNRFITEKTVDILKLSELDQKIYVTQSAIQDDNIAKASLFSLQLQLAHLLRFAPYP
                                                                                                           GVENRDSINRKVHGQLYAGFITHTIENRHWYTLQPNLVEFDITVPAKSIKYFVFRGRL
                                                                                                                                                                         HSPTLGEWYDKLNTNTSEWHTLFHNSMLIPKSLVSVLSLNNTVTVMVRHLERKNEHIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQYKVYTEIVYLSNQVAWRDAVMDPTSRYYIPPLVEEGKSATIIAGNTPLNVIMLRLL
DEDTPARISQNLAYKDYKIKLVGGKGGLTVQIGGGGTYTLTGDVSAKNTISFRAIPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AWVEYKQFLDSAAKLVVKAYPESHLLDLSGNRVLGNLYLDLSQNPPLLKGDVSRNYDS
LIGHVGDWSDRQVRNRLGYGYRSSPERALAKGHANTRWPREIPHIAKGVYETVYLGYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYYPELGWFVRGLNGLMVSHKGSAAVSHVIKGQQDAYQELAAMRQEVLSGEFFRSLED
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NFFNYCLLKGVGNISDETRMEYLEKELKFSKEEIEEYRKLKESNKEKIASVVKKLNEQ
LGSARVHIKDIKELNSMKHSQNIYNYEMEMFLRWNYAAATDQVRMYMLEEYGGLYTDL
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/db_xref="GI:7190481"
/translation="""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity; putative"
                                                                                                                                                                                                                       VDLSSLVPTFVRGRMTSQTVNGPSIDLEISSPRYTLPLQISWGSHVLPRNTRFDVMPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGVCFNLSNHAMQNVPMMRPNGTKIEALKIQQTGFSVIAGSAEGYDILTGEKDTHFYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTHRQHKDLIGGHLVSDYLAKSLFFDYRQDSIMPEAVSTLGITGPDLVAQKLVELFKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISRLTEEDKTKLGELFKELEFFVKKDTQNSSKLGKAKSFFQPMNMDIVRDTMPILRRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMMPAFSQEVLEVIKKHSVGDRMFEDMTSRRAISDAVLKLAVGETTTVSIEDIGKDID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSDKKGNEKKTEEKSKVSFIKDVADIIKAEFSGHLVPVDKIIHGIWIAGAPPEGIEQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mpvSgSIvASKENTSASLQPATTLNNGSSVEFFQQITVYDDARN
FTNHTTEDVIKIGEQLQRKFYNMTEGTQVPFTTSPAYHTGNWKTAFIYNLAQVIANLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLGLSSEQQTSVKELLNKLRKAITNYNALIEKNSSEGQSLLIRQAKLVEEIQEKISPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNIHNHTPDKKSSGESLRNISLEKPVLSRKRRDVEKNKEIKNEPSVNKYDLTYKNIAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSTIQPIRVNSTRSSPFSTNSSVEKRNRFTSKDTKVQPPHTTRSVSPRKRKSVIVTRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
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Db
                    δÃ
                                           DЬ
                                                               δÃ
                                                                                                Query Match
Best Local
                                                                                      Matches
                                            9518
  9578
                      70
                                                     10 taaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactga 69
CTGGCAAATTCGAGATAGAATAGGTTACGGTTATCGAATTTCTCCGAC 9625
            TAAAGGAGATCGCTCTTATAATTCTAATTGGAGAATAGGGAATAAGGCTGGTTGGACAGA 9577
                                                                                      60;
                                                                                                Similarity
                                                                                      Conservative
                                                                                                 25.4%;
                                                                                      0;
                                                                                                 Score 31.2;
Pred. No. 4;
                                                                                      Mismatches
                                                                                                           DВ
                                                                                      48;
                                                                                                          1;
                                                                                                           Length 23366;
                                                                                      Indels
                                                                                     0;
                                                                                     Gaps
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0;

CDS

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FEATURES
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AUTHORS
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REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone K10D6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-JUN-1996) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RO, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda;
Rhabditoidea; Rhabditidae; Pel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true left end of clone K10D6 is at 1 in this sequence. The true left end of clone T19B10 is at 30388 in this sequence. The start of this sequence (1. 108) overlaps with the end of sequence hL021173. The end of this sequence (30388. .30494) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erratum:[[published errata appear in Science 1999 Jan 1;283(5398):35 and 1999 Mar 26;283(5410):2103 and 1999 3;285(5433):1493]]
2 (bases 1 to 30494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortiun Science 282 (5396), 2012-2018 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neighbouring submissions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  White, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The C.elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     none
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; GABA receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans cosmid K10D6, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence Z74043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="K10D6.1"
join(1925 ~~~
                                                                                                                                                                                                                            Similarity to Drosphila GABA receptor beta subunit (SW:GAB_DROME), contains similarity to Pfam domain: PF00065 (Neurotransmitter-gated ion-channel), Score=148.6, E-value=5.7e-43, N=2
                           /translation="MLQIFLINISISFPLVIFSFIFQLLSMTLFLPNWCSGFYYHDDV
MLSSQMHNRKTPNSFFIFLILLSILQINICEIIIDSDYNVSSDDDPTTTTQKPRNCTR
QPAIIDKLLNGTGYNKFRIPNENGVPVQVEFWVQAITSINEITNDFEMDIYINEMWLD
PALKEDHLNPCKQNLSVSHQVLEQLWTPNSCFVNSKFAEIHDSPFKNVFLMIYPNGTV
                                                                                                                                            /protein_id="CAA98509.1"
/db_xref="GI:3878477"
                                                                                                                                                                                                                                                                                                                                                                            /gene="K10D6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(1925.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="K10D6"
                                                                                                                 /db_xref="SPTREMBL:Q21420"
                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                   /note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:1403245
                                                                                                                                                                                                                                                                                                                                                                                                    ln(1925. .2071,3486. .3705,3814. .3893,3953. .4045,
38. .4174,4480. .4528,4580. .4905,4954. .5404,5462. .5539)
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.4174,4480. .4528,4580. .4905,4954. .5404,5462.
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loderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consortium
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                                                    gene
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complement(join(6150...6262,6410...65
6977...7187,7236...7461,7969...8202))
/gene="K10D6.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(6150. .6262,6410. .65
6977. .7187,7236. .7461,7969. .8202))
/gene="K10D6.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEHHREWAWHKAILFFIITSEFLAFISICSGCAPCVPSTAFAFSISLFIAMLCSLLA
DGIFFLAANRVDNRFVQGMVGTYEQRIQYAFYLHLMGTLCWIGAFVCTLLTTYKEVTG
DEEDGSKENLFTWQQQTQPVTLSVNELPYRREEPLLHDKFVSSQQAGYRPNPQVPYRT
TSITQYRETSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mGSTVTQKLLLALSIVLILVGICLTSAGCFSPAWQVVDIREFRA
EHQHGLWWDCIRAEKHVVSVGDFYDETPLHCMYKFDNSAELVIQNTLNNIDEDGAAGE
SEHHRFWAWHKAILFFIITSEFLAFISICSGVCAPCVPSTAFAFSISLFIAMLCSLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EHQHGLMWDCIRAEKHVVSVGDFYDETPLHCMYKFDNSAELVIQNTLNNIDEDGAAGE
SEHHREMAHKALIFFIITSEFLAFISICSGVCAPCVBSTAFASISLEIAMLCSLLA
DGIFFLAANRYDNRFVGAMVGTYGARIGYAFYLHLMGTLCWIGAFVCTILTTYKFVTG
DEEDGSKENLFTWQQQTQPVTLSVLCVCFVFCWCASLSFQKIRRSSSAATTVSSQQQI
                                                       /translation="MSTQPSHPSSSNDLDSSIGTARIEVVSVPVKPRNKFSTTPVKRVENKKSKESDSVDKALKVKSSLDCMKLEKPAPTTCEMKAA"
                                                                                                                                                                                                                                                                                              /gene="K10D6.
join(13294. .
                                                                                                                                                                                                                                                                                                                                                                                                                    DG1FFLAANRVDNRFVQGMVGTYEQR1GYAFYLHLMGTLCW1GAFVCTLLTTYKFVTG
DEEDGSLCVCFVFCWCASLSFQK1RRSSSAATTVSSQQQ1NVDQL1FNFF1TFFLSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (join (6262, 6406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="K10D6.2c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(6262,6406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="CAA98514.2"
/db_xref="GI:6425186"
/db_xref="SPTREMBL:045670"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA EST yk255d4.5 comes from this gene cDNA EST yk526b2.3 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="cDNA EST yk284g4.3 comes from this cDNA EST yk284g4.5 comes from this gene cDNA EST yk525b5.3 comes from this gene"
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7236..7461,7969..8202))
/gene="K10D6.2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSLGTKAMPARTMLGVNALLAMIFQFGNIMRNLPRVSYVKAIDVWMLVSMTFIFLSLL
ELAIVGYKTKNEEGSKKKCPHKKLLDNFEASPAGLCRYEKRFMLPVERRSARWGGIIR
EQVFQDFWNWSPEKIDRYSAIMFPACFAITNIYWSYYNKKLEAEMKLNEDRL"
                                                                                                                                          /protein_id="CAA98510.1"
/db_xref="GI:3878478"
                                                                                                                                                                                                                                                                                                                                                         join(13294.
                                                                                                                                                                                                                                                                                                                                                                                           FESTHPSSIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB54276.2"
/db_xref="GI:6425185"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="K10D6.2c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVDQLIFNFFITFFLSLCFESTHPSSIKMSFHTEERSHCSTTNLYHHNKPAIGRTHRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EHQHGLWWDC IRAEKHVVSVGDFYDETPLHCMYKFDNSAELVIQNTLNNIDEDGAAGE
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/translation="MGSTVTQKLLLALSIVLILVGICLTSAGCFSPAWQVVDIREFRA
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/db_xref="GI:3878481"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WVNYRVNVKGPCDLSLELFPLDIQECHLIYESFNYNNQEVRMRWNEKSAEPVSVTNKI
                                                                                                                     /db_xref="SPTREMBL:Q21421"
                                                                                                                                                                                                                                    /note="predicted using Genefinder"
                                                                                                                                                                                                                                                                   /gene="K10D6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MGSTVTQKLLLALSIVLILVGICLTSAGCFSPAWQVVDIREFRA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="cDNA EST yk255d4.3 comes from this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=
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                                                                                                                                                                                                           _start=1
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   27902,
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                              .23550,23983.
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28159,28296.
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                              .24056,27146.
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                                 .27301,27401. .27463
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PUBMED REFERENCE

MEDLINE

TITLE JOURNAL

AUTHORS TITLE JOURNAL

COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGAACGGGAAGATTTATGTCCAAAGTAAGACTCATTTTTCATACTTTCCTCGGAACA 19719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTTTCAATCCAAATGCTCTTGGAATCTTTCTCACTAGTTCTCGGCTTGTAAAGTATGT 19660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               actgactggtaagtttcacatgtaaggtgatacttatcttcaatttattccacacaaca 123
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 83145)
Lin,X., Kaul,S., Rounsley,S.D., Shea,T.P., Benito,M.-I., Town,C.D., Fujii,C.Y., Mason,T.M., Bowman,C.L., Barnstead,M.E., Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M., Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., Vanaken,S.E., Umayam,L., Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
                                                                                                                                                                                                                                                                                                                          complete sequence. Sequence
AC002339 AE002093
AC002339.2 GI:6598350
                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thallana chromosome II section 226 complete sequence. Sequence from clones T3266,
                                                                                                                                                                                                                                                 Arabidopsis thaliana
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GOKFAQLNEKVMISHIVRNFKIEPTLKYNDTKPCLEVVTKPSNGIPVRLIRRN"
a 5582 c 5196 g 10100 t
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KRMMNFLDLMLSMEESNQLTSEDIRQEVDTFMFAGHDTTTSSTSWACWNLAHNPNVQE
KVYKEMIEVFGDDPNTDITLENVNNLNYLDIVLKESKRIIAPVPALQRKLTNDLEIDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGNLGPIVGKKTEDLPSVFINWAAEQRDQGHSVMRVMILGKVYAWPLNGKAAAAIIDS
TTETNKGDDYRFFDPWLGGGLLLEGYGERWKSHRKMLTPAFHFAKLGGYFEVFNNESK
LLIDLLSDFSASGETVDIFPYVKRCALDIISETAMGIKIDAQINHDHKYVQAVEGYNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Join(29944. .30048,30200. .30266,30347.
274043.1:108. .267,274043.1:318. .1008,2
/gene="T19B10.1"
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JOIN(2944. 30048,30200. 30266,30347. 30494,

Z74043.1:108. 267,Z74043.1:318. 1008,Z74043.1:1324. ...

/gene="T19810.1"
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IYYDKLHLSDDEDDCWISDTRGRVVPRRFNANNASDLFRSLENLKEVTVIMKDVNVKN
LOAMGPQNNTTECTPYTPGGYLOKLFGGISPSELHLROLSLHVDIMVESLEDVYCLVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA98515.1"
/db_xref="GI:3878483"
/db_xref="GFISBTRENEL:021424"
/translation="MTIFIPISIAIILAYLATWIPTLLKYKRHWQYGSKLPGPPAHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAA98512.1"
/db_xref="GI:3878480"
/db_xref="SFTRMBL:021423"
/translation="MPQVWERGQSYDTAPNLCSKYTSPHFTVQNIDSYPIMSSPSSTS
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(Cytochrome P450), Score=332.4, E-value=1.
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27716. .27902,27954. .28159,28296. .28568)
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6 of 255 of the
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,274043.1:1324.
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complete sequence against a peptide database and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, heter 1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prediction programs including GRAIL (ftp://arthur.epm.ornl.gov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.dk/services/NetGene2/), searches of the
                                    http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats were identified by repeatmasker (Arian Smit; http://ftp.genome.washington.edu/RM/RepeatMasker.html). Genes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genes were identified by a combination of three methods: Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medical Center Dr., Rockville, MD 20850, USA
On Dec 17, 1999 this sequence version replaced gi:2335089.
The sequence and annotation of chromosome 2 were merged from those
of the individual clones on this chromosome after removing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  overlaps. For detailed information, please see the TIGR web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (09-MAR-2000) The Institute for Genomic Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D., Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
    numbered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.tigr.org/tdb/at/at.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 402 (6763), 761-768 (1999)
20083487
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from the top to bottom of the chromosome.
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We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.

This work was supported by the National Science Foundation,

This work was supported by the National Science Foundation, Department of Energy and the US Department of Agriculture.

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                    misc_feature
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.>13035)
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CDS
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RFLPFVLMLLEYGLALASSTYCLTFFFTEHSMAQATSSYSVLLQHEFISLFVFSESNVIL
MVHFFSGLILMVISFVMGLIPATASANSYLKELLIRFYALQNIFFRLSPGFCFDGAS
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TMLYLQNLRXYYPGDKHHGPKVAVQSLTFSVQAGECFGFLGTMGAGKTTTLSMLSGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KTSPTVSVAAHIVHRHIPSATCVSEVGNEISFKLPLASLPCFENMFREIESCMKNSDS
DYPGIGSYGISVTLEEVFLKPAGCNLDIEDKOEDIFVSEDTKSSLVCIGSNOKSSMO
PKLLASCNDGAGVITTSVAKAPELIVAAVWTLIGFISTOCGGCSIISRSMEWRICKAL
FIKRARSACRDRKTVAFOFIIPAVFLLFGLLFULKFHPDQKSITLTTAYFNPLLSGK
GGGGPLPFDLSVPIAKEVAQVIEGGWIDPLRWTSYKFFNPKEALADAIDAAGPTIGPT
LLSMSEFLMSSEDQSYGSREGLSSHDSCHEPDGSLGYTVLHNGTCQHAGPTYLNWTH
LANLEFLATGNKNMTIQTRNHPLPPTKTQRIORHDLDAFSAAIIVNIAFSFIPASFAVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSKYPGRKKNNLQNRI DGFETDMFPADI EVNQGEPFDPVFESI SLEMRQQELDGRCI Q
VRNLHKVYASRRGNCCAVNSLOTIY YENQI LSLLGHURGAKKSTI SMLVGLLPPTSGD
ALILGNSI ITNNDEIRKELGVCPQHDILFPEILTVREHLEMFAVLKGVEEGSLKSTVVD
MAEEVGLSDK INTLVRALSGGMKRKLSLGIALIGNSKVI I LDEPTSGMDPYSMRLTWQ
LIKKIKKGRI I LLTTHSMDEAEELGDRIG I MANGSLKCCGSS I FLKHHYGVGYTLTLV
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DNVVTEKLVEFDLLKHSHKPSFTLSGGNKRKLSVAIAMIGDPPIVILDEPSTGMDPVA
KRFMWDVISRLSTRSGKTAVILTTHSMNEAQALCTRIGIMVGGRLRCIGSPQHLKTRY
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VRNGSNPKIKGAVVFHEQGPHLFDYSIRLNHTWAFAGFPNVKSIMDTNGPYINDLEMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITPDTASASEISLSPEMVQRIAKFLGNEQRVSTLVPPLPEEDVRFDDQLSEQLFRDGG
IPLPIFAEWWLTKEKFSALDSFIQSSFPGATFKSCNGLSIKYQLPFGEGGLSLADAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNHLELEVPFYNGVKPNEVSNVELENFCQIIQQWLFNVPTQPRSLLGDLEVCIGVSDS
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RAHVGLRWSNIWRASSGVSFFVCLLMMLLDSILYCALGLYLDKVLPRENGVRYPWNFI
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COMMENT
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                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                              human.
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72816 AATGAGAATTTCCACTCGGCAAAGATAGCCATGTGTATTTACAGAAGGCTTCTGGTCACT 72757
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Direct Submission Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Submitted (30-MAR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USJ On Apr 25, 2001 this sequence version replaced gi:8576174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 16 clone CTD-2519D12, WORKING DRAFT
                                                                                                                                                                                                                                  2 (bases 1 to 68575)
DOE Joint Genome Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           DOE Joint Genome Institute
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21547. .21679,21776. .21980,22070. .22175,22312. .23
23520. .23625,23720. .23892,23976. .24320))
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Complement(join(<20937. .21001,21098. 121218,21326. .214:
20547. .21679,21776. .21980,22070. .22175,22312. .23385,
23520. .23625,23720. .23892,23976. .>24320))
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MMDPYLPSLSIGLTNQMLHLFGKSGKVEAMMKLFYKIIASGVGINLKTYAILLEHLLA
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/note="T11A7.17; |
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Consensus quality: 43126 bases at least Q40
Consensus quality: 46452 bases at least Q30
Consensus quality: 46452 bases at least Q30
Consensus quality: 46452 bases at least Q30
Estimated insert size: 53000; agarose-fp estimation
Estimated insert size: 65075; sum-of-contigs estimation
Quality coverage: 8.56 in Q20 bases; agarose-fp estimation
Quality coverage: 6.98 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 36 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Submitted (14-MAR-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                         Published Only in DataBase (2001) In press 2 (bases 1 to 161818) Sasaki.T., Matsumoto,T. and Yamamoto,K.
                                                                                                                              Sasaki,T., Matsumoto,T. and Yamamoto,K. Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                                                                                       Oryza sativa (cultivar:Nipponbare) DNA,
                                                                                                                                                                                                                                                                           AP003409 161818 bp DNA
Oryza sativa chromosome 1 clone
PROGRESS ***, in ordered pieces.
                                                                Direct Submission
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/clone_lib="CalTech human B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mall:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 12, 2001 this sequence version replaced gi:13027286.
Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no. and RGP clone ID.
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Oryza sat
AP003256
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced
classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (cultivar:Nipponbare) DNA, clone:P0460E08 Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Only in Database (2001) In press 2 (bases 1 to 170020)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone: P0460E08
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/chromosome="1"
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                                                                                    identity or significant homology to a protein is
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Pred. No. 14;
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The orientation of the sequence is from T7 to SP6 of the PAC clone. Detailed information on overlap and assembly quality together with protein of the pacture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB61195.1"
/db_xref="GI:14597284"
/db_xref="GI:14597284"
/translation="MRADRLMAEGGKRIDLGAPLRSVRHADALPYHKADLNSGPVRHP
/translation="MRADRLMAEGGKRIDLGAPLRSVRHADALPYHKADLNSGPVRHP
GAVPFVWEQRPGQPKSVRTRRAPPSPTTASHPQPLEHGVEDEIDGSPYHDALGEHYVG
ILHGVDASPACSRTGAPAPAPARDEKRAQVAEAAVLQAKKEVTEKQVVSVAAVLRKGD
                                                                                 GLHKEYAITINSDGLFHGSQSCVGNLKSNFTGTKFTIRDWQPPYEGAKAFSSRSGRWF
GNKHRCPLVSTGDVEVGEVSYKYSLLRPRGPRRWSCSVQCPVLKGTAVDPQDGKRLSN
SIPSSLVLNSKVPSWHEHLQCWCLNFHGRVMVASVKNFQLIAPVEPGEPSDKTVVLQF
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YKHKLEQKYVRPGEDGRSKLTSESNQLTFWSDSQAGNGSSPFHHSAGGGLIECRTPVL
GVARPKREPARKFPPSITKREFARKFPPPSLGLDLLLYLKGLPHGPNNLT"
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                                                        GKIDDDVFTMDYRQPLSAFQAFAICLSNFGTKLA"
                                                                                                                                                                                                                  /product="putative Tub family protein"
/protein_id="sas61197.1"
/protein_id="sas61197.1"
/db_xref="GI:14587286"
/translation="MVPWRRSSSSSSAPSSRPARRPARTNARVSPDVSSELSPLAGEE
                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(17683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(17683. .18229,18366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDPEPHRVDASLAPNPSRRQPLLRPGKSTAFKREERRKRKERKQ
QERLALDLERWEPLGAPPRPAAAAASPSRÅALPDKPWVCDPPPEPEPSASWGCGWGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(15923. .16636,16711. .16809)
/gene="P0460E08.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDDDDEERFSDALDTLSRTESFTVNCSVSGLSGMPEPTSRAAAGAEAGVRGIMMDRFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRQRRRTRTCATMAARPWTWTLRRMQRRVARVHRLLRAGPRPRAMRTAGRLISRPLAP
SPLQLSRKSYMDLLSPIIVRPDNNWFYGCGLIHVCN"
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/gene="P0460E08.1"
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complement/7000
                                                                                                                                                                SGKITFPSSLKQPGPRDAPMQCFIKRNKKNSTFFLYLGLTQELTDDEKFLLAARRCRR
                                                                                                                                                                                               GAGEERWSALVPDLLADILRCVEAGSERWPPRRDVVACASVCRRWRDVAVAVVQPPLE
                                                                                                                                                                                                                                                                                                                                                                                     19584. .19925))
                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0460E08.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19584. .19925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FADAVGRLLGWSAGRTTALQMQTDSDNAGMCDEDIHCEDVPQSAEMEMCPHQ'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>AAEPPREPPVPAAVSPQAAAVEACRAFFGEHVDHDDGDDEDEEEEEGNVARFFQELLE</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB61196.1"
/db_xref="GI:14587285"
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/gene="p0460E08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(9680. .10489,10922. .11084,13870./gene="p0460E08.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MVAAVAEADEVGGDSCSGQGRRQRHTEATSMVDKDEGSGGRSGQ/
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/db_xref="GI:14587283"
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/chromosome="1"
                                                                                                                                                                                                                                                                                                                             /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                               .18229,18366. .18495,19014.
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  complement(join(39824.
41406. .41457))
                                                                                                                                                ITRLLDANPKTRITYPEIIESDWFKKGYKPVKFYIEDDKLYNLSDDVLNLEPADPVPP
PLGLAPPVPPPPQGDDPDGSGSESDSSVVSCPATLSTGESQRVRGSLPRPASLNAFDI
ISFSKGFNLSGLFEERGNEIRFVSGEPMSDIVKKLEEIAKVKSFTVRRKDWRVSIEGT
                                                                                                                                                                                                                                     KYELGRVLGQGSFAKYYQARHLETDECVAIKVLDKEKAVKGGMVHLVKREINVLRRVR
HPNIVQLFEVMASKTKIYFVMEYVRGGELFSRVSKGRLREDTARRYFQQLVSAVDECH
ARGVFHRDLKPENLLVDENGDLKVSDFGLAAGPDQFDPDGLLHTFCGTPAYVAPEVLR
                                                                                                                                                                                                                                                                                                                                                                                                complement(36914. .38476)
/gene="P0460E08.9"
/note="contains EST D48640(S14969)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB61200.1"
/db_xref="GI:14587289"
/translation="MRNNGPAADCRAVRHHKRRGALVARAGRHHCRGRPTMPPTDALT
CSYTSAKAAAAQQVQCEGSL"
CSYTSAKAAAAQQVQCEGSL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGDMSLVASAPSVLLARKEASQOHDDEEDDGFAREKKKRSNVIMSSPVIDVRPSSMNA
FDIISRSRGLDLSKMFDAEERRSEARFSTRETTTAIVSKLEEIAEAGRFSFKLKEKGR
VELEGSQDGRKGALAIEAEIFKVAPEVHVVEVRKTGGDSPDFRDFYKQELKPSLGDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLSRSPRFPEPVARRYFQQLITAVEFCHSRGVYHRDLKPENLLLDARGDLKVTDFGLS
ALDGGLRGDGLLHTTCGTPAYVAPEVLLKRGYDGAKADIWSCGVILFVLLAGYLPFNE
TNLVILYRNITESNYRCPPWFSVEARKLLARLLDPNPKTRITISKIMDRPWFQQATCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="OSPK4-like protein"
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/db_xref="GI:14587288"
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VFDKEAVQRSGTVEOVKREVDVMRRVHHRHVIKLHEYMATRSKIYFVMEYASGGELFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(28620. .30044)
/gene="P0460E08.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mrrahaQphGSrwntrTGGaDrGrPVPTSAGLAPTWRLRGCHVG
WREVDDDAGRNGRRTTAASGGANHGDTGENEHTGWLHETRGDEPTARIRRRKLDGGES
RRRQPAVGKGENGDEVTRGRFPAVRASTRPRESDASVGLGGATPSEAGDERVLRSSSG
                                                                 complement(join(39824.
41406. .41457))
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="P0460E08.9"
complement/260:
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join/34075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="P0460E08.6"
/note="rvob-''
                                         /gene="P0460E08.10"
                                                                                                                            REGVKGPLTIGAEIFELTPSLVVVEVKRKAGDNEEYEDFCNMELKPGMQHLVHQMLPA
                                                                                                                                                                                                               RRGYDGAKADIWSCGVILFALMAGYLPFHDHNIMVLYRKIYNGEFRCPRWFSKDFTRL
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/translation="MLMATVSPARREPTPQAVRASPMPSAAAALVRRGGGGSGGTVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(28620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0460E08.6"
complement/????
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/db_xref="GI:14587287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to Oryza sativa chromosome 10, OSJNBa0076F20.29"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0460E08.5"
/note="hw-----
                                                                                                                                                                                                                                                                                                                                                                /product="OsPK7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(34076. .34252,34827. .34844)
/gene="P0460E08.8"
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                     .39920,40576. .40677,41062.
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Best Local :
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962 TACCAGAATGACCCCCTACTGGTGCAGTGTGAAGGTTGGCCAAAATCTTTTGTTGAACCT 903
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                                                                                                                                                                                                                                         Rockville, MD, USA
Rockville, MD, USA
Rockville, MD, USA
This sequence was identified as CDM:10210186 by the submitter. For more information on this record e-mail to fly@celera.com.
**NOTE: This is a 'working draft' sequence.
** This sequence will be replaced
** by the finished sequence as soon as it is available and
** the accession number will be preserved.
**Coachion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
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HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                         Conservative
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/gene="p0460E08.11"

/note="probably inactive due to frameshift(s) in probably inactive due to stop codons(s) in CDS
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/gene="P0460E08.11"
complement(47319. .
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ADVRAVVRPCHHVPFGLSAHSGARPCRCVSTRTPEPPGSPFLPGDGAAPRDAGIFRFV
YAIWTGASSTAKHSALYYRVIDIQYLSKWTEEISGARNSFGNL"
                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /pseudo
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/db_xref="GI:14587291"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M. Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research, 320 Charles Street, Cambridge, MA 02141, USA 00, Jul 13, 2000 this sequence version replaced g1:6467063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein Howland, J.C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., McGurk, A., Mc
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                                                                                                                                                                                                                                                                                                                                                              overlap relationships among However, it should not be as
                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This record contains 82 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                      the record
                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome
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ject name: L3728
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10661: cor
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38021: contig of 8
3121: gap of 10
39018: contig of 8
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3721: gap of 100 bp
14582: contig of 861 bp
4682: gap of 100 bp
15537: contig of 855 b
5637: gap of 100 bp
16517: config of 856 b
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11625: ~
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20428: contig of
1528: gap of 1
21424: contig of
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37033: contig
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34119: contig of
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24369: contig of 902 bp
169: gap of 100 bp
25324: contig of 855 bp
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42068: contig
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35103: con
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23367: contig of 844
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 94797)
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Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and relationship to other sequences, please visit our seq archive Web site (http://fruitfly.berkeley.edu/sequence/) email to drosophila@mhgc.lbl.gov. Library locations: 45-68, 50-32.
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                                                                                                                                                                                                                                                                                                                                                                         source
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RS. Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
Roll, R.A., Evans, C.A., Gocayne, J.D., Amnatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A.,
Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M.,
Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D.,
Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
Phouanenavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F.,
Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M.,
Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.
Direct Submission
AL Submitted (30-UUN-2001) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US
Sequence submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Lbeywam, C., Jalali, M., Kruse, D., Li, P., Mattlei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Parleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanenavong, S., Pittman, G.S., Purl, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C. Zaverning of Drosophila chromosome 2L, region 25F-26X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon Rogers, Y., An, H., Baldwin, D., Banzon, J., Beson, K.Y., Busam, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterayota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 166441)
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                                     /clone="BACR48E14 (D1326)"
/clone=lib="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC library, partial EcoRI
pBACe3.6)"
                                                                                                                                                                                                                                                        /organism="Drosophila
/strain="y; cn bw sp"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                          /chromosome="2L"
           35803 c
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35579 g 47155 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JUN-2001
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                                                                           'n
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TITLE
JOURNAL
MEDLINE
REFERENCE

20196006

AUTHORS

Adams, M.D., Celniker, S.E., Gibbs, R.A.,

Rubin, G.M. and Venter, C.J.

(bases 1 to 259973)

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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Besson, K.Y., Bernos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunkov, B.C., Dunkov, B.C., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Eleister, C., Gabrielian, A.E., Garg, N.S., F., Karlen, A.E., Garg, N.S., F., Karlen, G.H., Ke, Z., Kland, P., Harris, M.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Hernandez, J.R., Ketchum, K.A., Kalush, F., Karpen, G.H., Ke, Z., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Liu, X., Mattel, B., McIntosh, T.C., McLeod, M.P., McPharson, D., Mcrkulov, G., Milshina, N.V., Mobarry, C., Moshrefi, A., Mount, S.M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.R., Nelson, K.A., Nixon, K., Nixo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashbunner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Welson, C.R., Gabor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Miklos,G.L., Abril,J.F., Agbayani,A., An,H.J.,
Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basu,A.
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1 (bases 1 to 259973)
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Pred. No. 17;
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COMMENT
FEATURES
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JOURNAL
                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
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Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7297008.
Location/ualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submission
                 /db_xref="FLYBASE:FBgn0031732"
complement(join(22734. .23763,23844. .24295))
/gene="CG11149"
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complement(join(19824. .20287,20339. .20411))
/gene="CG14007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKIALREIRLLKNLKHPNLVSLLEVFRRKRRLHLVFEFCELTVLHELERHPQGCPEHL
TKQICYQTLLGVAYCHKQGCLHRDIKPENILLTAQGQVKLCDFGFARMLSPGENYTDY
VATRWYRAPELLVGDTQYGTPVDVWAIGCLFAELVRGEALWPGRSDVDQLYLIRKTLG
                                                                                                                                                                                                                                                                    complement(join(<22642. .23763,23844./gene="CG11149"
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complement(<19824. .>20411)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(<19824.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QAAA IAAARDKSKTSNTSLPLLPSTQHHHHPHQDYVKLQPLNKNANLLHRTEHHLPT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWSCEKLTKHSYFDDYTAKQRELEHVNSLEAANLRQQQLASQQFMLATAAQQLQTGPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLPRHIQIFGQNEYFKGITLPVPPTLEPLEDKMPAKSQQNPLTIDFLKKCLDKDPTK
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                                                                                                                        /map="25F5-26A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="25F5-26A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBan0014007"
/db_xref="FLYBASE:FBgn0031731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="CT33563"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CG7236 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CG7236"
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join(16590. 16757,16815. 17687,17749. 17886)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="25F4-26A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="CG7236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <16590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'db_xref="FLYBASE:FBan0007236"
'db_xref="FLYBASE:FBgn0031730"
16590...>17886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="CG7236"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oin(<16590.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="CT22313"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .259973
                                                                                                                                                                      ement(<22642. .>24295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .16757,16815. .17687,17749. .>17886
gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .20287,20339. .>20411))
                                                                                                                                                                                                                                                                                                . 24295))
                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
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mRNA

AHSQLDECHEGKPLGHSAADEPRIVPMATYEHSCYGIYTSKPFVLTLEVISFDLERVS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<31796. .>33085)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSAAAWQPKEHPPMASLLDAWAPLLPSWVLDSVLEQLVLPRLVAGVQEWDPLTDTVPI
DSWVLPWHAILGSKLEEAVYPQIRSKLGIALRAWSPHDRSARAMLTPWQKAFPEEEMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAWEQHTRGIGAKLLLQMGYEPGKGLGKDLQGISHPVQAHVRKGRGAIGAYGPETAAS
IGGKTNKSIKVDEDVREAKEFKDQLNKWRKGSAGGAEPMERQGKRYYYKSVEEVIAKG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVGKLFCYIDRHVCMVSDGSFSNWKPVSLNHLLERSQTGIL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFLQRYIVPKLQATLGELIINPMHQDLELWQQVWEWHELIDPMYMAQLLDRHFFPRWM
QVLVVWLNQSPDYAEISRWYTGWKSMLSEPLLREPSVKEHLRRALEIMHRASDTLLQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LFDERVTWEGQSNKRIQVSYYCSQVSVSQCNLLLQNYAMCLLDYEYHVLSPAFLVHSP
GIKQSSKADSTRLQYAKEMTKEIKNKIEPEYRVLFGKNSACKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGQKSVGLLLSNESNPSRFSANFHLANDQHPKIIRREDSARTKELRSLLKCRDRSLRF
ERLQHGEFWLLQNLVMGRKSREVGCAESVTYTTNGDFTFFDNLEMVVSRWRAPVSFAI
HTPGYDLNTTLDAIRYVRNCLPESDSIKDWVSFHVYFPNQHMPEYVPYDEAEVLMYPH
                                                                                                                                                                                                   /db_xref="FLYBASE:FBan0014006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVTPTPPPPVPPAPVIMMDLIHPPAQLEFKELVSQQCADLGIIFAPLPGRREMGKQIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APACVFAMPELTHNLQLLVSQCEQQTTATDNQERECSSQQAALESEHRKLEETVQLER
NHTRTLEESLERVERLIDNPDLSLPQAERLFRELLVDVAAEFHEFGLADLAAGVTAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mSDNDYERFEITDYDLDNEFNINRPRGRQSRHQQIYGIWADDSE
EESGGEGGTKRRGRAARKPKDYTMPVNFVAGGIQQAGKKKKKALQADDEKGSQKEGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FLYBASE:FBan0007238"
/db_xref="FLYBASE:FBgn0024191"
join(25469._.25577,25629...27907,27971...28102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>db</u>
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AQVFHLKLCPTCHTIPGQEEWLNRTSRADDHLHVFSKALRKWKFRAWEPFYVSDNTEP
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/db_xref="GI:7297011"
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                                                                                                                                                                                                                                      codon_start=1/
                                                                                                                                                                                                                                                                     note="CG14006 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     map="25F5-26A1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="CG14006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FLYBASE:FBan0014006"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="CT33562"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKRELVQWQPLENPTEPLPLIKKWRGMLQQGDAAEQQPRNVFDPYSSLIWAGVMPSFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQGEESDDSAASGRPAFGQNDPGSSNSSSEEERPTLSRKQPSTTFQHRSHIASERNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="FLYBASE:FBan0007238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <25407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCTLANGSLVSPLYTQIPTTDSYKSRANLTYPINVGRNIARLATNTHFIFACDIELYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MATISFCNRKYVRLWPVLILFNVALLLVWRNLQQAQKLAASSNT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:7297012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAF52282.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="sip1 gene product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'gene="sip1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="sip1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="sip1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(25407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..>28124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .25577,25629. .27907,27971. .28124)
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CDS

gene

mRNA

length length

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 210404 TTATCTCATAAACTTAGCATCTAAATTGATACTTAATTAGCACTTACT 210357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jun 10, 2000 this sequence version replaced gi:7021826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer ET; 73% of reads Chemistry: Dye-terminator Big Dye; 27% of reads exambly program: Phrap; version 0.990319 Consensus quality: 151162 bases at least Q40 Consensus quality: 152443 bases at least Q30 Consensus quality: 152443 bases at least Q30 Consensus quality: 153249 bases at least Q20 recent circular programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs of the programs o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 4.08 in Q20 bases; agarose-fp Quality coverage: 4.69 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 155172)
Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert size: 177000; agarose-fp
Insert size: 154672; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:http://genome.wustl.edu/gsc/index.shtml
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Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
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                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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9366
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                  On Jan 13, 2001 this sequence version replaced gi:11878000. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | tttcacatgtaaggtgatacttatcttcaatttattccacaca 120
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57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA
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/db_xref="taxon:9606"
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Pred. No. 19;
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DB

Length 155172; Indels

503 others

46; 2

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Gaps

0

on chromosome 9, complete

17-JAN-2001

TREMBL;

Wp:, WORMPEP;

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JOURNAL
REFERENCE
AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGAAGTCTCTCGCTAGTATTGTGTGGGAGTCTAAGTTTATTT 136592
                                     Submitted (14-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,
                                                                                                                         Hattori,M., Ishii,K., Toyoda,A., Fujiyama,A., Yada,T., Totoki,Y., Direct Submission
                                                                                                                                                                                  Published Only in DataBase (2000) In press (bases 1 to 174815)
                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. Homo sapiens 174,815 genomic DNA of 18q23
                                                                                                                                                                                                                                                                                                                                                                                                        HTG;
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae: Homo.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 18
                                                                                                                                                                                                                                                                                                                                                                                                                         AP001390.2 GI:8117301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RP11-70L8 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VECTOR: pBACe3.6
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(bases 1 to 174815)
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sapiens DNA, clone:RP11-635B11.
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by restriction digest data"
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/db_xref="taxon:9606"
/chromosome="9"
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/clone_lib="RPCI-11.1"
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| Clone RP11-635B11 map 18q23, WORKING
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COMMENT
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* NOTE: This is a 'working draft' sequence. It currently * consists of 21 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Consensus quality: 159194 bases at least 040
Consensus quality: 167087 bases at least 020
Consensus quality: 170693 bases at least 020
Insert size: 172815; sum-of-contigs
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166715
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104698 114347: cont
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Contact: hattori@gsc.
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                                             122180: gap of
 128565: gap of 
135791: cont.
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173248 contig of
174815 contig of
                           128465: contig of 6285
                                                                                                                    547: gap of 100 bp 104597: contig of 9950 b
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83572: contig of 10229 bp in length
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73344. .83572
/note="assembly_fragment"
173349. .174815
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169157. .171527
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163616. .16661
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155677. .159193
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135892. .142934
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122181. .128465
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114448. .122080
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104698. .114347
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/db_xref="taxon:9606"
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ORGANISM
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J.,
Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C.,
Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J.,
Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S.,
Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
Theodore,J., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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                                                                                                                                                                                                                                                                on Jul 26, 2001 this sequence version replaced gi:14994291. All repeats were identified using RepeatMasker: Smit, A.F. A. 6 Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson, Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens chromosome 18 clone F
IN PROGRESS ***, 2 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                Submitted (07-MAY-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 18, clone RP11-635B11 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs
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                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bases 1 to 178056)
                                                                           Center clone name: 635_B_11
                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
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Primates;
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Pred. No. 19;
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nes 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGTGCTTTATGCACTTCATTAGCTTATAGAAAAATTGAAATGCTGCAATAATTGTAAAT 108939
Insert size: 195491; sum-of-contigs
Insert size: 183499; 21.0% error; agarose-fp
Quality coverage: 10.77x in Q20 bases; sum-of-contigs Quality
coverage: 11.71x in Q20 bases; agarose-fp
                                                                                                Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid: L08752; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Consensus quality: 195355 bases at least Q40 Consensus quality: 195464 bases at least Q30 Consensus quality: 195463 bases at least Q20 Consensus quality: 195483 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgesh: CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jul 17, 2001_this sequence version replaced gi:14596366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL449423.11 GI:14787534
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                       Center project name: bA14912
                                                                                                                                                                                                                                                                                                     Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                        Center: Sanger Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babbage, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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1 168134: contig of 168134 bp in length
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168235 178056: contig of 9822
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/clone_lib="RPCI-11 Human Male BAC"
/30884 c 34094 g 63393 t 100 o
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                --- Project Information
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Pred. No. 20;
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1022 bp in
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AL136230
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Best Local :
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57;
                                                                                                                                                                    The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw., SWISSPROF; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                             This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
                                                                                                                                                                                                                                                                                                                                                                                                                                               together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jul 14, 2000 this sequence version replaced gi:8574123. During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations
                                                               chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                annotated human repeat sequence elements (e.g. Alu). sequence is ambiguous, there is an annotation using
                                                                                                                                                                                                                                                                                                                                                                                                                          only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (28-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 120515)
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the accession number will be preserved
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1. .195491
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/clone="RP11-14912"
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCYPAC2
 /note="MIR repeat: matches 33.
                                                                                                                                                                  /note="16 copies 2 mer ac 87% conserved"
complement(10277. 10730)
                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(6082.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="31 copies 2 mer at 71% conserved"
complement(640 . .1130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="25 copies 2 mer aa 72% conserved"
complement(5063. .5482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9932. 4089
/note="LIMEc repeat: matches 890.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="match: GSS: Em:AQ595695"
751. .989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                              note="match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="match: GSS: Em:AQ530256"
                                                                                                                                                    note-"match:
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                                      note="AluJo repeat: matches 1. .298
                                                                             note="match:
                                                                                                                                                                                                                                                                                                                                    note="MER5A repeat: matches 50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluJo repeat: matches 59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       te="match: GSS: Em:AQ526871"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   te="match: GSS: Em:AQ511994"
                                                                                                                                                                                                                                                            e="MER5B repeat: matches 1. .173 of consensus"
                                                                                                                                                                                                                                                                                  ce="match: GSS: Em:AQ379073"
5. .6934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :e="L2 repeat: matches 2575.
7. .5951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ce="MLT1A2 repeat: matches 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    te="match: GSS: Em:AQ013144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .. .3929
.e="Alusg/x repeat: matches 134. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                         e="match: GSS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lement (5957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .4469
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                                                                                              .11289
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                                                                                                              GSS:
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                                                                         GSS: Em:AQ082251*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6576)
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Em: AQ630441"
                                                                                                              Em: AQ716569"
                                                                                                                                                  Em: AQ839431"
   .232 of consensus"
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                                                                                                                                                                                                                                                                                                                                      .161 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MLT2FB repeat: matches 1. complement(34176. .34667)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30430. .30896
/note="L1PA11 repeat: matches 5694. .6165 of consensus"
33041. .33473
                                                                                                                                                                                                                  38624. .38694
/note="AluJ/FRAM repeat: matches
                                                                                                                                                                                                                                                                          36513. .38620
/note="MER57-internal repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(12939. .13175)
/note="match: GSS: Em:B85743"
44326. .46056
/note="L1PA15 repeat: matches 2010. .3753 of consensus"
                                                                                        39339. .43921
/note="MER57-internal
                                                                                                                                            /note="MER57-internal repeat:
                                                                                                                                                                                                                                                         consensus"
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20444. .24195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLT2CB repeat: matches 1. .450 of consensus"
18954. .19430
                                  'note="MER57B
                                                                                                                                                                                   note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                   note="L1PA15 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                               /note="HAL1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="14 copies 2 mer ct 92% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="AluJo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="MIR repeat: matches 14. .241 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="match: GSS: Em:AQ429929"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="18 copies 2 mer tg 100% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MIR repeat: matches 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="match: GSS: Em:AQ835474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MER5A repeat: matches 9. .182 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .35696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copies 2 mer tt 62% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                             repeat: matches 1170. .1526 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 7851. .7977 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 2448. .6279 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 1.
                                                                                                                                                                                                                                                                                                                 repeat: matches 1. .399 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                          GSS: Em:AQ152633"
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                                  repeat: matches
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                                                                                          repeat:
                                                                                                                                                                                                                                                                                                                                                   matches 1910. .2012
                                                                                                                                                matches 2129.
                                    1. .403 of consensus"
                                                                                            matches
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RESULT 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morman, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Willey, R., Markey, R., Wo, A., Wheeler, J., Wu, X., Willey, R., Wo, A., Wheeler, J., Wu, X., Willey, R., Wall, R., Wo, A., Wheeler, J., Wu, X., Willey, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, W., Willey, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R., Wall, R.
                                                                                                                                                                                     Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 20, 2000 this sequence version replaced g1:9123835 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Conserv
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Birren,B., Linton,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C. and Lander,E Homo sapiens, clone RP11-11123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 159073)
                                                                                                                                                                                                                                                                                                                           Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Wyman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Contact: sequence_submissions@genome.wi.mit.edu
                                 Web site: http://www-seq.wi.mit.edu
                                                            Center code: WIBR
                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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complement(50343...
                                                                                                                                                                                                                                                                                                                                                                                    Ye,W.J., Zimmer,A. and Zody,M.
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/note="L1PA15 repeat: matches 5499.
49295. .49393
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~~ clone RP11-11123,
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                                                                                                                               -- Genome Center
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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S: Em:AQ894428"
. .50444)
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                                                                                                                       10 taaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactga 69
CTGGTATCTATTACTTGAAAATTTATAATAGACTTCAACCTAGTCCACATGAAA 4093
               ctggtaagtttcacatgtaaggtgatacttatcttcaatttattccacacaaca 123
                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently * consists of 5 contigs. The true order of the pleces * is not known and their order in this sequence record is
                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 156407 bases at least 040 Consensus quality: 158013 bases at least 030 Consensus quality; 158013 bases at least 020 Insert size: 157000; agarose-fp Insert size: 158073; sum-of-contigs Quality coverage: 5.6 in 020 bases; agarose-fp Quality coverage: 5.6 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                          52902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: L3173
Center clone name: 11_I_23
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134634 159073: contig of 24440 bp in length
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30689 820
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27848 c 26048 g
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82143. 108087
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment"
108188. .134533
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/clone="RP11-11123"
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134533: contig of 26346 bp in
34633: gap of 100 bp
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Pred. No. 23;
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sum-of-contigs
                                                                                                                                                                                                                                                                                                          401 others
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                                                                                                                                                                         Gaps
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Homo sapiens chromosome 4 clone RP11-352124 map 4, WORKING DRAFT SEQUENCE, 5 unordered pieces.

AC022863

159150 bp

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ACCESSION
VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13: M7915; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 157848 bases at least Q30 Consensus quality: 157848 bases at least Q20 Consensus quality: 158421 bases at least Q20 Insert size: 157000; agarose-fp Insert size: 158750; sum-of-contigs Onality coverage: 6.6 in Q20 bases; agarose-fp Onality coverage: 6.6 in Q20 bases; agarose-fp
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Choepel,Y., Colangelo,M., Collins,S., Collymore, Concept, S., Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore, Collymore,
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----- Genome Center
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center clone name: 352_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 6.6 in Q20 bases; agarose-fp Quality coverage: 6.5 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   preserved.
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J., Barna,N., Beckerly,R., Beda,F.,
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REFERENCE
AUTHORS
TITLE
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               E 2 (bases 1 to 170022)

E 3 (bases 1 to 170022)

E 4 (bases 1 to 170022)

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Berman, A., Burkett, G., Castle, A., Collego, S., Baldwin, J., Brown, A., Burkett, G., Castle, A., Coepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gauge, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Lieu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Machand, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Naylor, J., Naylor, J., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., McLey, B., McKernan, D., V., Martin, D., V., Martin, D., V., M., P., M., M., P., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCULLODY 1/0022 bp DNA
Homo sapiens chromosome 4 clor
SEQUENCE, 10 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens chromosome
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103061. .159150
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29976 c 29236 g 48959
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/clone_lib="RPCI-11 Human Male BAC"
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/chromosome="4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Vassiliev, H., Viel, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .159150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.7%; 56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .48389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29.2;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NA HTG 23-APR-20 clone RP11-753L19 map 4, WORKING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aum, C. and Lander, E. clone RP11-753L19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
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FEATURES
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                                              misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 23, 2000 this sequence version replaced gi:6814977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 161482 bases at least Q40 Consensus quality: 165432 bases at least Q30 Consensus quality: 167439 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 169122; sum-of-contigs Quality coverage: 4.3 in Q20 bases; agarose-fp Quality coverage: 4.4 in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66886

87091 87190; gap of

87191 108749; contig

108750 108849; gap of

142086; conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L5673
Center clone name: 753_L_19
-----Summary Statistics
Sequencing vector: M13; M77815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  142087 142186: gap of
142187 170022: cont
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66786 66885:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12622 12721: gap of 100 bp
12722 23152: contig of 10431 bp in length
/note="assembly_fragment"
52353. .66785
                                                                                                               /note="assembly_fragment"
                                                                                                                                                                                                                                                           /clone="RP11-753L19"
/clone_lib="RPCI-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                   /chromosome="4"
                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                            7 170022: contig of Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 23252: gap of
                                                                                                                                                             note-"assembly_fragment"
                                                                                                                                                                                                                                                                                                          /map="4"
                                                                'note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3847: contig of 3847 bp in length
3947: gap of 100 bp
12621: contig of 8674 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (16-JAN-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6785: contig of 100 bp
68795: contig of 14433 bp in length
885: gap of 100 bp
87090: contig of 20205 bp in length
190: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52252:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252: gap of 100 bp
37025: contig of 13773 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome
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contig of 21559 bp in
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Submitted (30-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 25, 2000 this sequence version replaced gi:7671263. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Alleu, Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Diaz, J.S., Collymore, A., Cooke, P., Dearellano, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart, K., Dewart,
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                                                                                                                                                                                                               Vassiliev, H., Viel, R.,
                                                                                                                                                                       Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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87191. .108749
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142187. .170022
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Pred. No. 23;
                                                                                                                                                                                                               Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
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                                                                                                                                                                                                                                                                                                                  38605 38704: gap of 100 bp 1 38705 4558: gap of 100 bp 45459 45558: gap of 100 bp 45559 52091: contig of 6533 bp in length 52092 52191: gap of 100 bp 52092 52191: gap of 100 bp 58656: contig of 6465 bp in length 58657 58756: gap of 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 1
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Insert size: 179427; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
Quality coverage: 4.7 in Q20 bases; sum-of-contigs
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Consensus quality: 172044 bases at least Q40 Consensus quality: 176527 bases at least Q30 Consensus quality: 178383 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                   17257 117356: gap of 100 bp
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39035 181127; contig of 42093
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2328 5041: contig of 2714 bp in length
5042 5141: gap of 100 bp
5142 8953: contig of 3813 hr. i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8953: contig of 3812 bp in length
4 9053: gap of 100 bp
4 13203: contig of 4150 bp in length
1 13303: gap of 100 bp
1 18520: contig of 6500
                                                            /chromosome="4"
/map="4"
          /clone_lib="RPCI-11 Human Male BAC"
                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                      /clone="RP11-683C4"
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31130: contig of 6795 bp in
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1 (bases 1 to 181542)
Birren,B., Linton,L., Nusbaum,C.
Homo sapiens chromosome 4, clone
Unpublished
                                                                                                                                                                                                                                                                 Homo sapiens chromosome 4 clone SEQUENCE, 23 unordered pieces. AC023187
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55; Conserv
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                     AC023187.2 GI:7139717
HTG; HTGS_PHASE1; HTGS_DRAFT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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139035. .181127
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99439. .117256
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52192. .58656
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RP11-102H15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Ferreira, P., Fitthugh, W., Forrest, C., Gage, D., Galagan, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 1, 2000 this sequence version replaced gi:69577
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (09-FEB-2000) Whitehead Institute/MIT Center for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. Anderson, S., Baldwin, J., Barna, N Boguslavkiy, L., Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stojanovic, N., Subramanian, A., Talamas, J., Tesfay Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roy, A., Santos, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nttp://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 23 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                     be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                    1 3660: gap of 100 bp 5983: contig of 2323 bp in length 4 6083: gap of 100 bp 4 8818: contig of 2735 bp in length 9 8918: gap of 100 bp 9 8918: gap of 100 bp 11436: contig of 2518 bp in length
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                                                                             22236:
                                                                                                                                                                                                  11536:
30436:
                                                                                 #041: gap of 100 bp
18297: contig of 3656 bp
8397: gap of 100 bp
22136: contig of 3739 bp
2236: gap of
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...: gap of
18297:
                                                    25665; contig of 3429
                                                                                                                                                                         14541: contig of 3005
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              contig of 4571
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J., Barna, N., Beckerly, R., Beda, F.
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Wu,X., Wyman,D.,
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74407 85102: contig of 10696 bp in length
85103 85202: gap of 100 bp
85203 95862: contig of 10660 bp in length
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65145. .74306
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14642. .18297
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25766. .30336
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/db_xref="taxon:9606"
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144833: contig of 17187 bp in length
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48303: contig of 9
403: gap of 10
55751: contig of 7
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111886: contig of 15924 bp in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gehrig, H.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V.aphylla mRNA for phosphoenolpyruvate carboxylase x91634
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-SEP-1995) H.H. Gehrig, TH-Darmstadt, Botanik FB10, Schnittspahnstr. 10, 64287 Darmstadt, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Vanilloid clade; Vanillaae; Vanilla.
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Vanilla aphylla
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                                                                                     /translation="SDSGKDAGRLSAAWPVYKTQEELVQVAKQFGVKLTMFHGRGGTV
GRGGGFTHLGILSQPDTILGSLRVTVQGEVIEQCFGEERLCFRTLQRFTVATLEHGM
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                                  ELVKLNPTSEYAPGLEDTLILTMKGIAA"
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                                                                                                                                                                            /product="phosphoenolpyruvate carboxylase"
/protein_id="CAA62828.1"
/db_xref="GI:2145479"
                                                                                                                                                                                                                                   /codon_start=1
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/EC_number="4.1.1.31"
                                                                                                                                                                                                                                                                                                           /gene="ppc"
                                                                                                                                                                                                                                                                                                                                             tissue_type="shoot"
                                                                                                                                                                                                                                                                                                                                                                  /organism="Vanilla aphylla"
/db_xref="taxon:53061"
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31041 c 31307 g 56823 t
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163055. .181542
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144934. .162954
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127647. .144833
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111987. .127546
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RESULT 4
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burgdorferi group.
1 (bases 1 to 17078)
1 (bases 1 to 17078)
1 (bases 1 to 17078)
Eraser,C.M., Casjens,S., Huang,W.M., Sutton,G.G., Clayton,R.,
Eathigra,R., White,O., Ketchum,K.A., Dodson,R., Hickey,E.K.,
Gwinn,M., Dougherty,B., Tomb,J.F., Fleischmann,R.D., Richardson,D.,
                                                                                                                                                                Borrelia
AE001152
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                                                                                                     Borrelia burgdorteri
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 14039)
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                                                                                    Bacteria; Spirochaetales;
                                                                                                                   Lyme disease spirochete.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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/db_xref="taxon:7227"
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melanogaster,
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Pred. No. 28;
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                                                                                       Borrelia
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DOMIKRAGKNIRDLKILSFDKLRVVDLFYAKNLIALESAVNKLNEFYIK" 56535964 /gene="BB0480" 56535964 /gene="BB0480" /note="similar to GP:1685373 percent identity: 100	gene CDS	/note-"hypothetical protein; identified by Glimmer; putative" /codon_start=1 /transl_table=11 /product-"B. burgdorferi predicted coding region BB0475" /protein_id="AAC66868.1"	
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/product="ribosomal protein L4 (rplD)" /protein_id="AAC66863.1" /db_xref="01:2688412"		. 0 > > `	gene
<pre>/note="similar to GP:1685372 percent identity: identified by sequence similarity; putative" /codon_start=1 /transl table=11</pre>		<pre>/codon_start=1 /transl_table=11 /product="B. burgdorferi predicted coding region BB0474" /protein_id="AAC68869.1"</pre>	
/gene="BB0479" 5018 5647 /gene="BB0479"	CDS	/gene="HBU4/4" /note="hypothetical protein; identified by Glimmer; putative"	
GRMGGNQQTIQNLEVVLIDEEKRALLVKGAVPGAKGSFVVVKKSKK" 50185647	gene		CDS
/translation="MLGLIXOKYOMYQIFQKMGTKVVYYYVITEKONYXIIKYVVYY YSALIAGSVDLKSSKYSKPIKGQYKSLKDIEVKRYVIELKGLIXOKYDAGDEIKVDV VKYVDYGTGTAGKTKOKYOKYOKYOKYOKYOKYOKYOKYOKYOKYOKYOKYOKY		₩ % H	gene
<pre>/product="ribosomal protein L3 (rplC)" /protein_id="AAC66864.1" /db_xref="GI:2688413"</pre>		YRLNYGLKIHLKDLVIDIRSIKEIVNLGLPSTFGQIMVSLSFFIFNYIVIEISPKFLA AYGLTNTIISFLFLPAMGIGTGIISIVGQNLGAKKVNRVEEVLKKGFFISLAILLIIN SIVIFNKQFILRLFTNDLEVLNYANNYLLLTTIGTFGYGLQQVFFGGLIGSGRTKIAM	
/Hote: Similar to SF.1003/1 Percent Adentified by sequence similarity; putative" /codon_start=1 /transl table=11		YVGKLGAMPLSALSLAGPVUFFILAIDMATGSISLASKEIGEGNESRESRYAGQLI VLNEVLSLEVTICAFFFIDHLLDLLGVKGELKELSRVYEYVTIFAIPIMELSISITYI LNAOGETILSMTIVLEANIVNEILDPILIESENMGITGAAMATLESKILTVVEYLELT	
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43885008 /gene="BB0478"	gene		
<pre>/protein_id="AAC66865.1" /db_xref="GI:2688414" /translation="MIAKDKIRVRLFSFDVKILDQSAESIVKAVQKAKAQIKGPI /translation="MIAKDKIRVRHFSFDVKILDQSAESIVKAVQKAKAQIKGPI TKIKKYTVLRSPHVNKKSREQFEMRTHKRLIDILEPTSALMDSLMKLELPAGVEV O"</pre>		<pre>/note="similar to SP:P54181 PID:1256651 GB:AL009126 percent identify: 23.93; identified by sequence similarity: putative" /codon_start=1 /trans1 table=11</pre>	
<pre>/transl_table=11 /product="ribosomal protein S10 (rpsJ)"</pre>			CDS
		× 1.11	gene
77" lar to GP:1685370 percen		/orga /db_x	
- p	CDS	Location/Qualifiers 1. 17078	FEATURES source
SGRILEILE" 4041 4352	gene	Submitted (12-DEC-1997 Medical Center Dr. Rock	JOURNAL
KLINKDAK ALKYEDI DINAPERKAK TI INARHI EYEKANI YA KUNONI HANDA KIKANI KANADA KAN		Richardson, D., Peterson, J., Kerlavage, A. R., Quackenbush, J., Salzberg, S., Hanson, M., van Vugt, R., Palmer, N., Adams, M. D., Gocayne, J. D., Weidman, J., Utterback, T., Watthey, L., McDonald, L., Artlach, P., Bowman, C., Garland, S., Fujil, C., Cotton, M. D., Horst, K., Roberts, K., Hatch, B., Smith, H.O. and Venter, J.C.	T T T T T T T T T T T T T T T T T T T
/product="translation elongation factor TU (tuf)" /protein_id="AAC66866.1" /db_xref="GI:2688415"		2 (bases Fraser,C. Lathigra,	REFERENCE AUTHORS
/codon_start=1 /transl_table=11		Nature 164. Nature 30 (6660), 580-586 (1997) 9 98065943	JOURNAL MEDLINE
/note="similar to GB:LZ3125 PID:34940/ SP:P50062 PID:1685369 GB:AE000783 percent identity: 100.00;		Venter, J.C. et.al. Genomic sequence of a Lyme disease spirochaete, Borrelia	TITLE

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ISIYCS
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(GPIPLP

TVDRDG (VDVFKS 'KGTKMA

SYRLPK SYRLPK ILLGND

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SOURCE
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AE002717
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Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X.,
                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 4975)
                                                                                                                                                                               fruit fly.
Drosophila melanogaster
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5986. .6819
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identified by sequence similarity; putative"
/codon_start=1
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GGYAMILASDGNYVTVKLSSGEMRLIFKKCIATIGEIGNEDYANISIGKAGKSRWLGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSSGRISIRRRGGGHKRKYRLIDFNRRDKFSIPARVASIEYDPNRSANIALLVYKDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC66861.1"
/db_xref="GI:2688410"
/translation="Worse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mlrismkayDiivSpmLtektnTQRESinvyvfkvnkrankkEv
GaaikELfnVTPvSCNLLNIKSkakvvvSrkGypiGkGkTSSwkkayvyLkkEDkiDi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="BB0482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BB0482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPKVRGVAMNPVDHPHGGGEGKTSGGRHPVSPWGQPTKGYKTRKKKRYSDKFIIKRRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="BB0483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="BB0483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   identified by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to GP:1685374 percent identity: 98.92;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'codon_start=]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MGIKTYKPKTSSLRYKTTLSFDDLSKGNDPLKSLTKGKKFKSGR/
                                                                                                                                                                                                                                                                                                                       melanogaster
                                                                                                                                                                                                                                                       GI:7289774
                                                                                                                                                                                                                                                                                                                                               49759 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.8;
Pred. No. 28;
                                                                                                                                                                                                                                                                                                                     genomic scaffold 142000013385965, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GP:1685375 percent identity: 97.83;
uence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 17078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                            06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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REFERENCE
AUTHORS
TITLE
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JOURNAL
MEDLINE
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Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
Muzny,D.M., Nelson,D.L., Nelson,M., Pittman,G.S., Pan,S.,
Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R.,
Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,
Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
Zhong,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
NE 20196006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M., Bodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferriera,S., Fleischmann,W., Fosler,C., Gabriellan,A.E., Garg,N.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadleu, E., Center, A., Chandra, I., Busam, D.A., Butler, H., Cadleu, E., Center, A., Chandra, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rockville, MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gabor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 49759)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <8107
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                                                                                                                                                                                                                                                        /codon_start=1
/db_xref="FLYBASE:FBan0017570"
                                                                                                                                                                                                                                                                                                                                                                                               8107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="FLYBASE:FBan0017570"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="39E1-39E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <8107. .>8511
/gene="CG17570"
                                                                                                                                                                                                                                                                                                                       /note="CG17570 gene product"
                                                                                                                                                                                                                                                                                                                                                      /gene="CG17570"
                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="CG17570"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CT34146"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="2L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
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.16286
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RESULT 44
AC004735/c
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AUTHORS
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ORIGIN
                                                                                                                                                      REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Locus
                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12852 TGGGGAACTGGTGGTACAAAGCCAGGGGCTCAGTTAGTGTTAAGTCCATCAAGTGAGCAG 12793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                            Celniker, S.E. Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, Butenhoff, C., Champe, M., Chavez, C., Chew, M., Cicsiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Poon, L., Punch, E., Sequeira, A., Sethi, H., Snir, Svirskas, R.R., Twomey, B., Wan, K.H., Weinburg, T., Zhang, R.,
                                           Celniker,S.E., George,R.A., Galle,R., Svirskas,R.R., Hoskins,R.A., Agbayani,A., Arcaina,T.T., Baxter,E., Blanzerj,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,
                                                                                                                     Celniker, S.E., George, R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster, chromosome 2L, region 38A7-38C9, Pl clon DS04178, complete sequence.
AC004735 AC004119 AC000718 AC000719 AC000720 AC000721 L81497 AC0001816 L81498 AC000722 AC000723 AC001208 L81499 L81496 AC000724 AC000725 AC000726 AC000727
                                                                                                                                                                                              Zieran,L.L. and Rubin,G.M.
Sequencing of Drosophila chromosome 2L, region 38C
                                                                                                                                                                                                                                                                                                                                                                                                                                                Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fruit fly.
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                                                                                                                                                 (bases 1 to 74534)
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<15476. .>16286
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FKYHEGYNSKLMINDVAIIKLSSPVRQTSKIRAIELADSEAVSGTNAVVSGWGTTCFL
FCSSPDTLQKVEVDLLHYKDCAADTYNYGSDSILETMVCATGEKKDACQGDSGGPLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLYBASE:FBgn0032947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="CG17571"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74534 bp
Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.4%;
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Pfeiffer, B.,
                                                                                                                                                                                                                                                                                                                                                  Kearney, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                         Blazej, R.G
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                                                                                                                           requests: clonerequest@sanger.ac.uk

n Oct 1, 2000 this sequence version replaced gi:9931221.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.bearkeley.edu.
Pl library locations: 44-50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
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Zieran,L.L. and Kimmel,B.E.
Direct Submission
                                                                         as follows. An attempt is made to resolve all sequencing
                                                                                                      This sequence has been finished according to sequence map criteria
                                                                                                                                                                                                                                                                                                                                         Submitted (30-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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/clone_lib="P1 library, partial Sau3A in pAd10sacBII"
/clone_1552 g 21437 t
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/strain="y2; cn bw sp"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: RMBL; SW:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6

Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6

RP3-472A9 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RP3-472A9 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.

The true right end of clone RP3-472A9 is at 85195 in this sequence.
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/clone_lib="RPCI-3"
14629 c 16180 g 29459 t
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/db_xref="taxon:9606"
/chromosome="6"
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tive 0; Mismatches
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Copyright (c) 1993 - 2000 Compugen Ltd
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es 58; Conservative
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990S-0121825

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01-APR-1999;
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17-SEP-1999;
                                                                                                                                                                                                                                                                   The present invention relates to a recombinant DNA construct of a plant (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors \mathbf{f}_{i} the construction of transgenic plant and animal cells -
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Pred. No. 3
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3.1e-07;
15;
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11; 21;

Indels

Gaps

0;

53

Length 1082138;

G;

343444

Τ;

0 other;

for

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AAX20248/c
ID AAX20248 standard; DNA; 910715 BP
XX
AC AAX20248;
XX
DT 04-MAY-1999 (first entry)
XX
Borrelia burgdorferi; spirochete;
KW epidemic relapsing fever; endemic
KW epidemic relapsing fever; endemic
KW epidemic relapsing fever; endemic
XX
Borrelia burgdorferi.
XX
Borrelia burgdorferi.
XX
Borrelia burgdorferi.
XX
W09858943-A1.
XX
W09858943-A1.
XX
XX
W09858943-A1.
XX
XX
O3-SEP-1997; 97US-0050359.
PR 20-JUN-1997; 97US-00503344.
PR 22-JUL-1997; 97US-00503377.
XX
XX
XX
O3-SEP-1997; 97US-00503344.
PR 22-JUL-1997; 97US-00503377.
XX
XX
C1-1997; 97US-00503344.
PR 22-JUL-1997; 97US-0050334.
PR 22-JUL-1997; 97US-0050334.
PR 22-JUL-1997; PR 22-JUL-19
     RESULT
AAC49264
ID AAC
XX
AC AAC
XX
DT 18-4
                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                           406528
                                                                                                                                                                                                                              406588
                                                                                                                                                                                                                                                                                                                                                                                                                            AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the productton of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrelia burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease
       18-OCT-2000
                                        AAC49264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.
                                                                        AAC49264
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                                                                                                                                                                                                                                                             σ
                                                                                                                                                                            tattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgc
                                                                                                                                                         AAATAATCTTATTTTTGACAGAAATGGTTATAAGTATCATGGACTTATTGCA
                                                                                                                                                                                                                            TATTGATGATGTAAAAAAAACTTGGAGAAGTTCTTGCTAAAAAGGCTTAAGGAGAAAAAATAT 406529
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                                                                        standard;
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       (first
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     entry)
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Pred. No. 11;
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16-APR-1999;
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23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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RESULT 12
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ID AAC45107
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Best Loc
Matches
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    Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                       Arabidopsis
                                                                          AAC45107;
                                                        18-OCT-2000
                                                                                                                                    327
                                                                                                                                                                              Local
                                                                                                                                  Match
                                                                                                                                                                    ch 23.1%;
l Similarity 76.1%;
35; Conservative
                                                                                         standard; DNA; 1474
                                        thaliana
                                                        (first
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9908-0151133
9908-0151333
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                                                        entry)
                                        DNA
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21-JUN-1999
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RESULT 13
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XX DE CDNA S
XX Human;
KW Human;
KW immune
XX immune
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13-OCT-1999;
13-OCT-1999;
                                                                                                                     cDNA sequence encoding a human phosphorylation effector PHSP-30.
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                                                                                                                                                                                                                                                                                                                                                   CGATGGCTCCTCTGACTGGGAGGTTCTTCCTTGCGGTTGTTGTTCCCCCAACAATTTCTTC
                                                                         phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                             ch 21.5%;
l Similarity 61.8%;
42; Conservative
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                           870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9908-015659
9908-0156596
9908-015717
9908-0157865
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9908-0158029
9908-0158232
9908-0159293
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19908-0159633
19908-0159633
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9908-0160741
9908-0160768
9908-0160768
9908-0160815
9908-0160815
9908-0160815
9908-0160815
9908-0161406
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9908-0161360
9908-0161361
9908-0161361
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99US-0154039.
99US-0154779.
99US-0155139.
   Location/Qualifiers 62..1132
                                                                                                                                                                                                                CDNA; 2347
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0; Mis
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No. 8
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              Homo sapiens
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RESULT 14
AAH15633/c
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Best Local Similarity
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14-OCT-1998;
03-NOV-1998;
19-NOV-1998;
22-DEC-1998;
12-JAN-1999;
12-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ46138-Z46168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, lumnune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
Human; primer;
                                    Human
                                                                     26-JUN-2001
                                                                                                                                             AAH15633 standard; cDNA; 2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 141-142; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human phosphorylation effectors useful for the diagnosis, treatment and prevention of proliferative, immune and neuronal disorders \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-183125/16.
P-PSDB; AAY68798.
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Reddy R, Lu DAM,
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                                                                                                          AAH15633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2347 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with increased PHSP expression/activity.
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                                                                                                                                                                                                                                agatgaaaaataccttcaagctat 117
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                                  sequence SEQ ID NO:13969
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                     (first entry)
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Bandman O, Au-Y
DAM, Shih LL;
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98US-0152814

98US-0173482

98US-0106889

98US-0109093

98US-0113796

99US-0173482

99US-0229005
detection; diagnosis; antisense therapy; gene therapy;
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/product= "phosphorylation effector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 A; 442 C; 454 G; 706 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                              21.5%;
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Au-Young J, Gorgone
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Pred. No. 10;
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gone GA,
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Yue
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H, Azimzai
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RESULT 15
AAX20838
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                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in complication. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs aesily without any specialised methods. AAH03166 to AAH13628 and CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CDNAs and AAH13629 to AAH13629 to AAH13632 represent human amino acid sequences; and AAH13629 to AAH13632 represent inventions.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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11-JAN-2000;
02-MAY-2000;
                         05-MAY-1999
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Ishii
                                                                 AAX20838;
                                                                                                      AAX20838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                          tattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgc 64
                                                                                                                                                                                                                            actgactggtaagtttcacatgtaaggtgatacttatcttcaattt 110
                                                                                                                                                                                                                                                                                     TAGAGCACAGGAGAAAGGTCTTAAAACCCTGGGCTTATGGGACGTTACCACGGAGACTGC 1280
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Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2620
                                                                                                      standard;
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                         (first
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                                                                                                      DNA;
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T, Wakamatsu
                       entry)
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                                                                                                      634
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A, Nagai K,
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15;
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C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                50;
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                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 16
AAV52156/c
ID AAV521
XX AAV521
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Best Local S
Matches 40
                                                                                                                                                                                                                      computer
                       31-OCT-1996;
                                                                                                    07-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                  AAV52156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        348
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AAX20500-21243 represent polynucleotide sequences from the genome Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidu infections, particularly syphilis. They can also be used for detections experience to Borrelia infections in animals, and for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
                                    30-OCT-1997;
                                                                                                               WO9818931-A2
                                                                                                                                                   Streptococcus
                                                                                                                                                                                                            Streptococcus
                                                                                                                                                                                                                                                  Streptococcus
                                                                                                                                                                                                                                                                                                                                                                   AAV52156 standard; DNA; 7147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 929; 1150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequence from the genome of Treponema pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                408 atat 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 ttat 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctatgagaattctgcactttctactcaattttacttggaaactcaaactgttctaaaaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gcaatgcgagggctgcactgactggtaagtttcacatgtaaggtgatacttatcttcaat 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-081273/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production;
                                                                                                                                                                                        readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                   pneumoniae
                                                                                                                                                                                                                                                  pneumoniae genome fragment SEQ ID, NO:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENOME SCI INC
96US-0029960
                                    97WO-US19588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0050667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US13041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 A; 127 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; syphilis;
ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.8%;
                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25.6; D
Pred. No. 13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 G; 155 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection; animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
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CDS	OS Helicobacter pylori. XX FH Key Location/Qualifiers FT CDS 3891579	<pre>KW Bordetella pertussis; VIR B4; Agrobacterium tumefaciens; invasion factor; KW Bordetella pertussis; VIR B4; Agrobacterium tumefaciens; invasion factor; KW vaccine; treatment; duodenal; gastric ulcer; active gastritis; KW adenocarcinoma; ss.</pre> XX	CagI locus.	AAT46159 standard; AAT46159; AAT46159;			Query Match 20.8%; Score 25.6; DB 19; Length 7147; Best Local Similarity 70.8%; Pred. No. 29; Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;	Sequence 7147 BP; 2088 A; 1641 C; 1265 G;	CC Iragments OI the S. pneumoniae genome OI commercial importance, or CC expression modulating fragments of the S. pneumoniae genome. Products CC from the present invention can be used in diagnosis kits and assays, and CC pharmaceutical compositions and vaccines for S. pneumoniae.	CC primers derived from the fragment of the S. pneumoniae genome to prime CC the amplification and isolating the amplified sequences. The computer CC readable medium can be used in a computer-based system for identifying	CC Indiany which contain sequences that hybridise to the target sequence and CC isolating the nucleic acid molecules from the members; or (b) isolating CC mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid CC molecules whose nucleotide sequence is homologous to amplification	CC of the sequences in SEQ ID No:1 to 391, identifying members of the	CC Streptococcus pneumoniae. The present invention also describes an CC isolated nucleic acid molecule encoding a homologue of any of the CC fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the			XX XX PS Claim 1; Page 289-293; 1409pp; English.		DR WPI; 1998-272225/24.	AA PI Barash SC, Choi GH, Dillon PJ, Dougherty BA, Fannon M; PI Kunsch CA, Rosen CA;	PA (HUMA-) HUMAN GENOME SCI INC.
ET CDS	FT FT CDS	FT CDS			FT CDS FT FT	FT CDS		भ भ भ भ । भ भ भ भ	FT CDS	FT CDS	FT CDS	FT CDS	FT CDS		FT CDS	FT CDS	FT CDS	य भा भ जे ने ने	FT CDS	FT
/note= "putative open reading frame; no start given" complement (1386614129) /*tag= s	₹,	/*tag= p /*tag= p /*tag= p /*tag= p /*tag= p /*tag= given" complement (1274313420)	complement (9/84103/3) /*tag= 0 /note= "putative open reading frame; no start given"	<pre>complement (89779762) /*tag= n /note= "putative open reading frame; no start given" 10575.</pre>	<pre>complement (84968918) /*tag= m /note= "putative open reading frame; no start qiven"</pre>	<pre>complement (79758454) /*tag= 1 /note= "putative open reading frame; no sta given"</pre>	71780 ve open	<pre>/*tag= j /note= "putative open reading frame; no sta given"</pre>	<pre>/*tag= i /note= "putative open reading frame; no sta given"</pre>	e ,	<pre>/note= "putative open reading irame; no sta given" complement (62186613) /*tag= h</pre>	given ment (55086233) h	<pre>complement (30203259) /*tag= g /note= "putative open reading frame; no sta</pre>	<pre>/*tag= f /note= "putative open reading frame; no sta</pre>	<pre>/note= "putative open reading frame; no sta</pre>	given complement (17782173) /*tag= e	44885426 /*tag= d /note= "putative open reading frame; no sta	<pre>/*tag= C /note= "putative open reading frame; no s given"</pre>	4 :	D

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RESULT 1
AAZ88746
ID AAZ8
XX
XX
AC AAZ8
AC AAZ8
AC AAZ8
AC AAZ8
AX AC AAZ8
XX
XX
AC AAZ8
AC AAZ8
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                                                                                                                                                                                                                                                                                     В
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                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                          The present sequence is the complete nucleotide sequence of the CagI C locus, including the true 5'-terminus of CagI. The sequence was CC constructed using overlapping clones (one of which also overlaps with CC the CagA region). The CagI region contains clusters of putative open CC reading frames (ORFS) with different polarities. The putative ORFS for CC this region are shown above. It is hypothesised that some of these ORFS for CC may encode exporter molecules with homology to the ptl genes of CC may encode exporter molecules with homology to the ptl genes and CC Salmonella pertussis and VIR B4 genes of Agrobacterium tumefaciens and CC salmonella genus. The absence of the CagA gene in the type I strains is CC associated with the absence of the CagA gene in the type I strains is CC fragments and encoded proteins are used in the diagnosis of H. pylori (esp. H. pylori type I strain) infection in an individual and in vaccines CC claimed) for the treatment of H. pylori infection associated with e.g.
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                  8085
           A. dichotoma
                                  18-MAY-2000
                                                                                                                                      8145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori CagI polynucleotide and related proteins in diagnosis and in vaccines for the treatment of H. pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
20-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                        AAZ88746;
                                                                              AAZ88746 standard; DNA;
                                                                                                                                                                                                                                                                                   Sequence 19932 BP; 6677 A; 3635 C; 3483 G;
                                                                                                                                                                                                                                                                                                         gastritis) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 3A-R; 303pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Covacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9633274-A1
                                                                                                                                                                                                                                                                                                                      duodenal and gastric ulcers, severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection associated disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOC-) BIOCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-OCT-1996
                                                                                                                                                           71
                                                                                                                                                                                            11 aaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac 70
                                                                                                    18
                                                                                                                                                 1996-485780/48.
DB; AAW06930-50.
                                                                                                                                   cgttaaattcccctgttaatttgctaatatttaagatattgttccccacagc
                                                                                                                                                                               aaatgcttgcaatctgactattaacagcaccaatttgcgcgccttggctgttgccttgag
                                                                                                                                                                                                                               58;
                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                              Conservative
           kabutosin A DNA
                                (first entry)
                                                                                                                                                                                                                                                                                                         gastric adenocarcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0477451
95US-0425194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-IB00343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (19296..19832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                        20.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "putative open reading given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "putative open reading given"
                                                                              591
                                                                              ВP
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                        Score 25.6;
Pred. No. 4:
                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                     forms of active
                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                   DΒ
                                                                                                                                                                                                                                                                                   6137
                                                                                                                                                                                                                                                   17;
                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame;
                                                                                                                                                                                                                                                                                   Η;
                                                                                                                                                                                                                                                 Length 19932;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                    gastritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        start codon
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                   (esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                  QΥ
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RESULT 19
AAH179
XX AAH179
XX AAH179
XX AAH179
XX AAH179
XX 26-JUN
XX Human
XX Human;
XX Human;
XX EP1074
XX EP1074
XX EP1074
XX EP1074
XX EP1074
XX EP1074
XX 28-JUL
XX 29-JUL
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes two novel peptides which have antibacter: activity, designated kabutosin A and B and which have been isolate Allomyrina dichotoma. The peptides are used as food preservatives and medical antibacterial agents. This sequence encodes the A. dichotoma kabutosin A protein described in the method of the
                                                        07-FEB-2001
                                                                                   EP1074617-A2
                                                                                                                                      Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
 29-JUL-1999;
                            28-JUL-2000;
                                                                                                             Homo sapiens
                                                                                                                                                                 Human cDNA sequence SEQ ID NO:17797.
                                                                                                                                                                                              26-JUN-2001
                                                                                                                                                                                                                         AAH17997;
                                                                                                                                                                                                                                                   AAH17997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 591 BP; 183 A; 123 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 9-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A new peptide, an antibacterial agent, a recombinant DNA and preparation of a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-176990/16
P-PSDB; AAY51547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NORQ ) NORINSUISANSHO SANSHI (NODA ) ZH NODA SANGYO KAGAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2000026499-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allomyrina dichotoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kabutosin A; kabutosin B;
medical; ds.
                                                                                                                                                                                                                                                                                                                      359
                                                                                                                                                                                                                                                                                                                                                                           299
                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                             catgtaaggtgatac
                                                                                                                                                                                                                                                                                                                                                                        cctctaatgttgaac
                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                             2000EP-0116126
                                                                                                                                                                                              (first entry)
                                                                                                                                        detection; diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0197190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98JP-0197190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 82..516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                   CDNA; 2333 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                            20.7%;
                                                                                                                                                                                                                                                                                                                      373
                                                                                                                                                                                                                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "kabutosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial; food preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25.4;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KONCHU.
KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                new peptide gene,
peptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Τ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                        gene therapy; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a new
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      82
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RESULT 20
AAA92497
ID AAA924
XX
AC AAA924
XX
DT 17-JAN
XX
DE Haemop
XX
KW Hia; a
KW non-ty
KW antiba
KW diagnc
XX
KW diagnc
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 47; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                           1487
                                                                                                                                                                                                                                                                                                                                                                              1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 represent human anino acid sequences; and AAH36246 to AAH3633 represent human anino acid sequences; and AAH3629 to AAH3632
                non-typeable Haemophilus influenzae; antiinflammatory; auditory; antibacterial; meningitis; epiglottitis; septicaemia; otitis media; diagnosis; immunogenic; antigen; ds.
                                                                                                                                            17-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least Is nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                   Hia; adhesin;
                                                                                                                                                                               AAA92497;
                                                                                                                                                                                                                 AAA92497 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set
                                                                                                      Haemophilus influenzae adhesin (Hia) gene from NTHi strain K9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2333 BP; 699 A; 427 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represent oligonucleotides, all of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                 27
                                                                                                                                                                                                                                                                                                                                                                                                    TAAGCTGAAGGTCAGATTCAAAT 1465
                                                                                                                                                                                                                                                                                                                             taaggtgatacttatcttcaatt 109
                                                                                                                                                                                                                                                                                                                                                                            ACTGCACAGACCCTGTACTGGCACAAGTTGATGGGTCCACTGGAAAAGAAATGCCCAAATA 1488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID 17797; 2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                            (first
                                                                 Haemophilus influenzae adhesin; NTHi; infection; vaccine;
                                                                                                                                                                                                                 DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nishikawa T,
                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25.4; DF Pred. No. 24; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of which are used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         791 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2333;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                   CC gene from the non-typeable Haemophilus influenzae (NVHi) strain ky.

CC Hia genes and proteins have antiinflammatory, auditory and antibacterial contivities, and can be used in the production of a vaccine. An excine and composition comprising an Hia gene, a polypeptide encoded immunogenic composition comprising an Hia gene, a polypeptide encoded by an Hia gene, or a recombinant Hia polypeptide is useful for inducing contection against disease caused by Haemophilus strains in a context of the context preferably a human. An Hia protein is useful as an excine context preferably a human. An Hia protein is useful as an experimental context preferably a human. An Hia protein is useful as an experiment of the generation of diagnostic reagents. Hia context of the immunogens, and in the generation of diagnostic reagents. His context is useful for treating diseases caused by the infection of Haemophilus confidence as meningitis, epiglottitis, septicaemia and otitis media. Recombinant production of Hia favours hip recovery of the protein compared to the low recovery of native protein from Haemophilus confidence species. A truncated protein has a significantly higher amount of recovery than a full-length protein.
                                                                                                              Matches
                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                         Sequence 3300 BP; 1099 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a Haemophilus influenzae adhesin (Hia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 22; 275pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acid e use as antigens and infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-2000; 2000WO-CA00289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CONN-) CONNAUGHT LAB
                                  154 agtgcttctgttacgagtaggttgaatgtttatggcgatacgaatactaaattcaatgca 213
                                                          57 agggctgcactgactggtaagtttcacatgtaaggtgatacttatcttcaattttattcca 116
                                                                                                              41;
                                                                                                                                Similarity
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0268347
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                                                                                                                                20.7%;
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                                                                                                                                                                                                         606 C;
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                                                                                                              0;
                                                                                                                              Score 25.4;
Pred. No. 27;
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                                                                                                                                                                                                         819
                                                                                                                                                                                                         G; 776 T; 0
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                                                                                                              26;
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                                                                                                                Indels
                                                                                                                                                 Length
                                                                                                              0;
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117 cacaaca
214 gccaata
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220
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RESULT 21
AAH839422 s
XX
AC AAH83942;
AC AAH83942;
XX
DT 25-SEP-200
XX
DE Callithria
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Olfactory
KW Olfactory
KW aromas; pe
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Callithria
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OS Callithria
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OS Callithria
                                          Callithrix jacchus
                                                                                    Olfactory receptor;
                                                                                                               Callithrix jacchus olfactory receptor encoding gene 10
                                                                                                                                            25-SEP-2001
                WO200146262-A2
                                                                      perfumery;
                                                                                                                                                                                                     standard; DNA; 649 BP
                                                                                                                                          (first entry)
                                                                      toxic substance;
                                                                                     human;
                                                                                    food processing industry;
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RESULT 2
AA160262
ID AA16
XX AA16
XX AA16
XX Huma
XX Huma
KW Perii
KW A1zi
KW A1zi
KW A1zi
KW Leul
XX Leul
XX Homo
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XX Homo
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XX PPD 26-1
XX X PP
PD 26-1
XX 25-1
PR 25-1
PR 21-1
PR 09-1
PR 19-1
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Best Local S
Matches 42
21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to olfactory receptors (AAG98432-AAG98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection of toxic substances and/or trapping of odours).
                                                                                                       WO200153312-A1
                                                                                                                           Homo
                                                                                                                                                                                                                    Human polynucleotide
                                                             26-DEC-2000;
                                                                                   26-JUL-2001
                                                                                                                                                                                                                                                            AAI60262;
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for analysis o
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                                                                                                                                                leukaemia;
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                                                                                                                                                                                                                                                                               AAI60262 standard; cDNA; 3684 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CNRS )
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21-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     649
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          2000US-0488725.
2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        s encoding primate and murine olfactory receptors, useful odours e.g. in food processing and perfumery -
                                                             2000WO-US34263
                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CENT NAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0171746
2000US-0747155
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                                                                                                                                                                                                                                                                                                                                                      70
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Pred.
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No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The the
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Wang
                                                                                                                      misc_feature
                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                       mycobacteria;
                                                                                                                                                                                                                                                                                                               BCG deletion
                                                                                                                                                                                                                                                                                                                                                                                                         AAT33537;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000; 2000US-0662191
19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                                                                                                                           15-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhao
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                                                                                                                                                                                                                                                                  delta
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DB; AAM41106.
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as central nervous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYSEQ INC
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                                                                                             virulence;
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                                                                                                                                                                                            bovis strain
                                                                                                                                                                                                                                          vaccine;
                                                                                                                 Location/Qualifiers 1406..10673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO 4251; 10078pp;
                                                                        /note=
                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            970
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  data
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                                                                                                                                                                                                                                                                                                           3 and flanking sequences
                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                        "BCG
                                                                                                                                                                                                                                          infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 5%;
                                                                                                                                                                                                                                                               avirulence; attenuation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides, useful system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human nucleic acids (AAI57798-AAI61369) and (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                            BCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.2; DI
Pred. No. 33;
0; Mismatches
                                                                        delta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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Xu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            c;
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                                                                        L
                                                                                                                                                                                                                                       marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.2; 1
No. 33;
                                                                     deletion region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma
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AJ,
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Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22;
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                                                                                                                                                                                                                                                             gene deletion;
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WO9625519-A1

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RESULT 24
AAH32402/c
ID AAH324
XX AAH324
XX AH324
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DT 30-JUL
XX Human
XX Second
KW Second
KW Secont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This DNA sequence comprises Mycobacterium bovis BCG deletion Sequence BCGdelta3. A specific genetic deletion of this region C results in an avirulence phenotype of the mycobacterium. 2 Other C deletion regions (see AAT3535 and AAT33536) have also been detected. C rediction involved screening a BCG cosmid library with a CC radiolabeled probe obtained following DNA subtraction between CC virulent Mycobacterium tuberculosis H37Rv and avirulent BCG.

CC The deletions provide useful markers for the identification of an CC avirulent, or a virulent, mycobacterial phenotype. Determination CC avirulence requires the detection of the presence or absence of the deletion; the deletions are detected either by detecting the CC presence or absence of deletion junctions (see AAT33538-46), or by CC detecting the presence or absence or absence of the sequences contained within CC the deletion. Deletion polypeptides are used as components of CC immunological assays and in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                         08-OCT-1999; 99US-0158615
24-FEB-2000; 2000US-0184809
                                                                                                                                                                                                                                                                                              Human; olfactory receptor; OR;
secondary scent determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5990 gacatggctttcaacgccgatgtcggtatggcgacctgcaaacgctgtggtgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting markers for avirulence in Mycobacterium - used in production of vaccines against bacterial infection, and to detect
                                                                                                                     06-OCT-2000; 2000WO-US27582
                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                      Human olfactory receptor polynucleotide, SEQ ID NO: 975
                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32402 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 66pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mahairas GG,
(DIGI-) DIGISCENTS. (YEDA ) YEDA RES &
                                                                                                                                                            19-APR-2001
                                                                                                                                                                                                 WO200127158-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 gagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac
                                                                                                                                                                                                                                                                           profile;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                           t determination; polypeptide library; odour r scent fingerprint; scent representation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0390878
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  & DEV CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25.2;
Pred. No. 50;
                                                                                                                                                                                                                                                                                                                   primary scent determination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 17;
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                                                                                                                                                                                                                                                                                            receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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Best Local
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                  US5861498-A
                                                                          polyA_signal
                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAX0441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                 polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       474
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receptors that are involved in detecting such secondary scents. This enables the construction of a scent representation (also called a scent fingerprint or scent profile), which may be used to re-create
                                                                                                                                                                                                                                                                                scents and the identification of the odour receptors used to detect these primary scents. The methods also enable determination of secondary scents and the identification of combinations of odour
                                                                                        and edit scents. Libraries of olfactory receptors are useful for determining the interaction pattern of a composition with the receptors, and can be used for determining differences in the olfactory faculties
                                                                                                                                                                                                                                                                                                                                                                           The present sequence is one of a number of isolated polynucleotides which encode polypeptides involved in olfactory sensation. The polynucleotides can be used in screening for olfactory agonists and antagonists. The methods allow for the determination of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8; Page 569; 1857pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists - \,
                                                              of different individuals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bellenson
   933
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   B₽;
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   206
   A.
   267
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   187
   G;
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   273
   ∓;
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   other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yanai I;
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DB 24;

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Length

0

Spodoptera frugiperda polyA_signa. polyA_signal transplant; 27-APR-1999 AAX04441 standard; cDNA; 2284 Immunophilin; moth; insect cell; nuclear; 414 TTTCA 410 61 ctgca 1 caggtattgtaaatgtgagatgccttacaacccctgatgacctaatggcgcaatgcgaggg frugiperda immunophilin FKBP46 cDNA. CAGGGAATGTAGGTGGGAGATGCTGCAAGAACCCAATAGCATGAGTAGGCAATGCCATGG 415 l Similarity 40; Conserv 65 tissue graft; Conservative (first entry) 1868..1873 /product= 1764..1769 1850..1855 160..1398 Location/Qualifiers /*tag= /*tag= 20.3%; ds "immunophilin FKBP46" 0 Score Pred. Mismatches No. immunosuppression; drug; 25; Indels 0; Gaps 60

/*tag= 2052...

..2242 ..2057 g= e

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RESULT 26
AAX23518/c
ID AAX235
XX AAX235
XX AAX235
XX AMINOP
CONTROL Human
XX AMINOP
KW Prenat
KW Prenat
KW Protei
XX WO9911
XX WO9911
XX WO9911
XX U1-MAR
XX PF 02-SEP
XX O2-SEP
XX O2-SEP
XX MEDI-
XX MEDI-
XX MEDI-
XX MPI; 1
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Best Local
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                                                                                                                                                                                                              prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis; arterial stenosis; industrial protein feed; malabsorption syndrome; proteinaceous waste degradation; additive; immunohistochemistry; ss.
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                                                                                       02-SEP-1997;
                                                                                                                                         11-MAR-1999
                                                                                                                                                                W09911799-A2
                                                                                                                                                                                                                                                                                                                                                         AAX23518 standard; DNA; 49998
                                    Ryan JW,
                                                                                                                02-SEP-1998;
                                                                                                                                                                                                                                                       Aminopeptidase; human; AmP;
                                                                                                                                                                                                                                                                              Human kidney
                                                                                                                                                                                                                                                                                                                                 AAX23518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the cDNA encoding the immunophilin FKBP46 from the moth Spodoptera frugiperda. FKBP46 is a novel insect cell nuclear immunophilin, which can be used to study and identify additional immunosuppressive drugs that bind to it. Such immunosuppressive agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated immunophilin FKBP46 nucleic acids - useful for developing products for the study and identification of immunosuppressive agents for treating e.g. transplant and tissue graft patients
                                                                                                                                                                                                                                                                                                        23-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2284 BP; 803 A; 373 C; 495 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           can be used in treating transplant and tissue graft patients.
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31-OCT-1996;
                                                             (MEDI-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                    cactgactggtaagtttcacatgtaaggtgatacttatcttcaat 108
                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      TAGACAACAATGTGGTATACCTGCAATATTTTACTGATGTTCAAT 1651
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55; Conserv
                                                             MEDICAL COLLEGE GEORGIA RES
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                                    Sprinkle TJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                              aminopeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JEFFERSON
                                                                                       97US-0057854.
                                                                                                                98WO-US18426
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96US-0741134.
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52.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THOMAS
                                      Venema RC
                                                                                                                                                                                                                                                      gene therapy; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25; DB Pred. No. 33; 0; Mismatches
                                                                                                                                                                                                                                                                              P genomic DNA fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                             INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      613 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
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                                                                                                                                                                                                                                                     AmP-deficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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AAH13128/c
ID AAH131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes the isolation of a novel human aminopeptidase P (AmP). This protein is used to produce recombinant AmP and can be used for gene therapy for treating AmP-deficiency conditions. Its fragments are used as primers and probes to identify patients with homozygous and heterozygous AmP deficiency, including prenatal diagnosis (patients defective in AmP are at risk of developing angioedema if treated with angiotensin-converting enzyme inhibitors), also as antisense inhibitors in cases of excessive AmP expression. The product of the invention is also used to identify AmP-expressing sequences in other animals and to generate transgenic animals, and comparisons of genomic sequences are used to detect mutations. AmP inhibitors are potentially useful as antihypertensive agents and to prevent or treat arterial (re)stenosis or atherosclerosis. The structure of AmP is used to design synthetic substrates, e.g. for use in AmP assays. AmP, which hydrolyzes N-terminal inion acids, to degrade to degrade industrial protein feeds to free amino acids, to degrade proteinaceous wastes, as additives in enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                         Ota T,
Ishii S,
                                                       Ota
                                                                                      (HELI-) HELIX RES INST.
                                                                                                                                                                                                         28-JUL-2000;
                                                                                                                                                                                                                                      07-FEB-2001
                                                                                                                                                                                                                                                                   EP1074617-A2
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                             Human; primer;
                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (3'-primer) SEQ ID NO:9963
                                                                                                                                                                                                                                                                                                                                                                                                                     AAH13128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH13128 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biological role. Antibodies against {\tt AmP} are used in immunohistochemical methods to study {\tt AmP} distribution.
                                                                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 49998 BP; 12605 A; 11725 C; 11351 G; 14317 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid encoding human aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               formulations used to treat malabsorption syndrome and for studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tggtaagtttcacatgtaaggtgatactt 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aaalgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac
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                                        Isogai T,
, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 109-139; 201pp; English
                                                                                                                99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                         2000EP-0116126
                                                                                                                                                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
                                         Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
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Pred.
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                                         Hayashi K,
A, Nagai K,
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95;
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                                         Saito K,
Otsuki
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                                            Η.
                                                          Yamamoto
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to free
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WPI; 2001-318749/34.

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RESULT 28
AAC39501/c
ID AAC395
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Best Local S
Matches 41
  25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                           Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC39501 standard; DNA; 1448
                                                                                                                            25-FEB-2000;
                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                              Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 gtgatact 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                        2000EP-0301439
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99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
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0; Mismatches
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99US-0144352 99US-0144632

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RESULT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA sequence SEQ ID NO:15679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUN-2001
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99JP-0300253.
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                                                                                                                         2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                       detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         521 A; 416 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA; 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     397 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         448 T; 0 other;
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RESULT 31 AAQ80535 ID AAQ805

AAQ80535 standard; cDNA to mRNA; 2064

ВP

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1936 taaatact 1943

91

gtgatact 98

1876 cctcgaagacgttgtgcctcacagcgaggcctacaagggatgggaacttttatttcaaaa 1935

Query Match Best Local Matches

41;

Conservative

0;

27; 22;

Indels Length 1970;

0;

Gaps

90

Similarity

20.2%;

Score 24.8; Pred. No. 37; Mismatches

DB

31-MAY-1996 AAQ80535

(first entry)

transglutaminase; fish;

Paralichthys olivaceus transglutaminase gene

Theragra chalcogramma;

Paralichthys

production; Pagrus major;
olivaceus; Oncorhynchus keta;

recombinant

Paralichthys olivaceus

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the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH83633 represent human amino acid sequences; AAB92446 to AAH3633 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                        to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 \, \mathrm{full}-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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09-JUN-2000; 2000JP-0241899
Sequence 1970 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; SEQ ID 15679;
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                                         of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ishii
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, Sugiyama T, Wakamats
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  434 A;
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  538 C;
    552
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  G; 446 T;
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  other;
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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                          A fish-originated trans:glutaminase amounts at low economic cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The DNA encodes a protein, isolated from Paralichthys olivaceus, which has transglutaminase (TG) activity. The TG's of the invention can be isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical to produce in large quantities.
                                                                                                                                 Claim 10; Page 49; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transglutaminase; fish;
Theragra chalcogramma;
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-100948/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paralichthys olivaceus transglutaminase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAQ80533;
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Paralichthys
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Pred. No. 37;
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olivaceus;
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Oncorhynchus keta;
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TG's of the invention can be

Sequence 2148

BP; 578 A; 496 C; 610 G;

464 T; 0 other;

transglutaminase

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RESULT 3
AAQ46026
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Best Local S
Matches 44
                                                                                                                                                                                                                          14-JAN-1992;
27-JUL-1992;
08-DEC-1992;
                  Transglutaminase is used in the prodn. of gelatinous food prods., cosmetics and chemicals. The DNA fragment enables the mass prodr of transglutaminase which is cheap and efficient.
                                                          The difference in the 1882 th
                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                               and chemicals
                                                                                                                      New gene encoding trans:glutaminase prodn. of trans:glutaminase for use
                                                                                                                                                      WPI; 1993-259983/33.
P-PSDB; AAR39519.
                                                                                                                                                                                    Matsui
                                                                                                                                                                                                                                                                   14-JAN-1993;
                                                                                                                                                                                                                                                                                     18-AUG-1993.
                                                                                                                                                                                                                                                                                                        EP555649-A.
                                                                                                                                                                                                                                                                                                                                                                   Paralichthys olivaceus
                                                                                                                                                                                                                                                                                                                                                                                                Transglutaminase; TGase; fish; Pagrus major; Alaska pollack; Theragra chalcogramma; Paralichthys olivaceus; paste; kamabo
                                                                                                                                                                                                                                                                                                                                                                                                                             Transglutaminase (fish liver)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ46026 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical to produce in large quantities.
                                                                                                                                                                                                       (AJIN ) AJINOMOTO KK
                                                                                                                                                                                                                                                                                                                                                                                      gelatinous
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                                                                                                                                                                                   Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                          Page 42-44; 85pp;
                                                                                                                                                                                   Motoki M,
                                                                                                                                                                                                                                                                                                                                                                                       food; cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                         92JP-0005166.
92JP-0199803.
92JP-0328010.
                                                          between the sequences of AAQ46025 and AAQ54878 base. The change does not alter the translated
                                                                                                                                                                                                                                                                  93EP-0100488
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/*tag= ;
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                          English
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RESULT 34
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                                                                                                                                                                                                                       Sequence 2148 BP; 578 A; 496 C; 611 G; 463 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               The difference between the sequences of AAQ46025 and AAQ54878 resides in the 1882 th base. The change does not alter the translated
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 45-47; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1993-259983/33.
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27-JUL-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New gene encoding trans:glutaminase prodn. of trans:glutaminase for use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAR39519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transglutaminase (fish liver) (G1882)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-1994 (first entry)
  661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              721 gactggtcagtggcac 736
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                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chemicals
tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 720
                            tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gactggtaagtttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 720
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                                                                                                    44;
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                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92JP-0005166.
92JP-0199803.
92JP-0328010.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
26..2092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ramma; Paralichthys olivaceus; paste; kamaboko;
cosmetic; ss.
                                                                                                                      20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase
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                                                                                                                      Score 24.8;
Pred. No. 38;
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pagrus major; Alaska pollack;
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nakanishi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from fish - for the in gelatinous food,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14;
                                                                                                                                             DB 14;
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                                                                                                 Indels
                                                                                                                                             Length 2148;
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cosmetics
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                                                                                                                      RESULT :
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AAQ80536
ID AAQ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The DNA encodes a protein, isolated from Paralichthys olivaceus, which has transglutaminase (TG) activity. The TG's of the invention can be isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A fish-originated trans: glutaminase gene - amounts at low economic cost.  \label{eq:cost} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarray}{ll} \end{subarray} % \begin{subarr
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31-MAY-1996
                                                                                         AAQ80534 standard; cDNA to mRNA; 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2148 BP; 578 A; 496 C; 611 G; 463 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-100948/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUL-1993;
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                                              AAQ80534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 54-56; 94pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transglutaminase; fish; recombinant production; Pagrus major; Theragra chalcogramma; Paralichthys olivaceus; Oncorhynchus keta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paralichthys olivaceus transglutaminase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ80536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to produce in large quantities.
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||||||||||||||
721 gactggtcagtggcac 736
                                                                                                                                                                                                               721 gactggtcagtggcac
                                                                                                                                                                                                                                                                                                                    661 tgtctatgtcagcaggatgatcactgcgatggtgaactctaacggtgacaggggtgtgct 720
                                                                                                                                                                                                                                              68 gactggtaagtttcac
                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                8 tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                        44;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       20.2%;
                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 24.8; D
Pred. No. 38;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                 ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 other;
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Best Local S
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                                               antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorde neurological disease; infection; human; secreted means.
                                                                                                                                                                                                                                                                                                                                                                                                The DNA encodes a protein, isolated from Paralichthys olivaceus, wh has transglutaminase (TG) activity. The TG's of the invention can be isolated from Pagrus major, Theragra chalcogramma, Paralichthys olivaceus or Oncorhynchus keta. Fish-originated TG's are economical to produce in large quantities.
           WO200055198-A1
                                Homo
                                                                                                                  Human secreted protein cDNA sequence
                                                                                                                                         30-JAN-2001
                                                                                                                                                              AAC59911;
                                                                                                                                                                                   AAC59911 standard;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 2148 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 50-53; 94pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A fish-originated trans:glutaminase amounts at low economic cost.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transglutaminase; fish;
Theragra chalcogramma; 1
                                                                                                                                                                                                                                    721 gactggtcagtggcac
                                                                                                                                                                                                                                                                                 661
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                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                      8
                               sapiens.
                                                                                                                                                                                                                                                                                            tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact
                                                                                                                                                                                                                                                          gactggtaagtttcac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1995-100948/14.
                                                                                                                                                                                                                                                                                                                         Similarity 57.9
                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0172998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
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                                                                                                                                                                                                                                                                                                                                                                               578 A; 496 C;
                                                                                                                                                                                 cDNA; 452
                                                                                                                                                                                                                                                                                                                                    20.2%;
                                                                                                                                                                                                                                                           83
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Paralichthys
                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                               610
                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
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olivaceus; Oncorhynchus keta;
                                                                                                                    #
5
                                                                                                                                                                                                                                                                                                                                                                               464 T; 0 other;
                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be produced in large
                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                         32;
                                                                                                                                                                                                                                                                                                                                              Length 2148;
                                                                                                                                                                                                                                                                                                                         0;
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RESULT 3
AAF26556.
ID AAF2
XX AAF2
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XX DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosts, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relate to the isolation of genes AAC59907-C59956 encod 50 human secreted proteins AAB28707-B28751. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G FC portion for increasing the stability of the fusion protein as compared to the human protein only. The genes proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 200
P-PSDB;
                                                                                                                      Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ss.
                                                                                         Homo sapiens.
                                                                                                                                                                                     DNA encoding
                                                                                                                                                                                                                     27-MAR-2001
                                                                                                                                                                                                                                                  AAF26556;
                                                              WO200076531-A1
                                                                                                                                                                                                                                                                              AAF26556 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 452 BP; 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 315; 391pp; English.
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23-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                       209 tcactgttcagtgtcacttgtttggtaacactcaacatcaacgtgtgctaccaaa
                                                                                                                                                                                                                                                                                                                                                                          67 tgactggtaagtttcacatgtaaggtgatacttattcttcaatttattccacacaa 121
                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-587520/55.
DB; AAB28706.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted proteins and ne therapy protocols an
                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
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                                                                                                                                                                                     human secreted
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99US-0166989
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Pred. No. 26;
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                                                                         New DNA sequences for - with secretion of pr transformed fungi
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29-AUG-1985;
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disease and
       Example; Fig 13; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                  (GENE-) GENENCOR INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (including leukemia), autoimmune diseases, allergies, inflamm graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) an involving abnormal angiogenesis, neurodegeneration and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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he cells, and new vectors an
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   control viral gene expression in
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*866666668*
The invention provides the primary nucleotide sequence of the WSBV genome (AAH62889), predicted transcript sequences (AAH62689-AAH62839) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to
                                                                                                                                                                                                                                Primary nucleotide sequence of the shrimp white spot Bacilliform (WSBV), useful for producing viral polypeptides that can be used screen for agents that are useful for treating WSBV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shrimp white spot
antiviral agent; g
transgenic viral r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungi is claimed. Pref the DNA sequence codes for bovine preprochymosin, M. meihei preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which
                                                                                                                                                                                           Claim 4; Figure 3; 626pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200138351-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           White spot syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                       (PENY-) PE CORP NY.
(THIR-) THIRD INST OCEANOGRAPHY
(SINO-) SINOGENOMAX CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 aggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggc 61
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)B; AAG85016.
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Pred. No. 4
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RESULT 'AAH81775
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Matches 42
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                                                                                       effects of an active compound (potential pharmaceutical) on a cell line, particularly for diagnosis and treatment of tumors, especially by modulating expression of (I) (by gene therapy, antisense RNA or ribozyme methods) or by modulating the amount and/or location of (I)-encoded polypeptides (by administration of the polypeptide or its activator, antibody (optionally as a conjugate) or inhibitor). The method allows identification of many Class II tumour suppressor genes (i.e. genes that are not primary targets for tumour-initiating mutations).

AAH81492-AAH82376 represent the human and rat derived nucleic acid fragments described in the method of the invention.
                                                                                                                                                                                                                                                       This invention describes a nucleic acid (I) with differential expression between tumour and normal cells and which has cytostatic activity. (I) work as modulators of Ras activity by inducing expression of tumour work as
                                                                                                                                                                                                                                                                                                                                                    Nucleic acids differentially expressed between useful for diagnosis or therapy of tumors and \boldsymbol{f}
                                                                   Sequence 3787 BP;
                                                                                                                                                                                                                                                                                                              Disclosure; Page 438-439; 579pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                         Grips
                                                                                                                                                                                                                            suppressor genes. (1), and polypeptides encoded by them, are useful as targets for diagnosis or therapy and in screening to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Differential transcription; human; rat; tumour cell; cytostatic; Ras modulator; Class II tumour suppressor gene; gene therapy; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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  l Similarity
42; Conserv
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33; Conservative
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Hellriegel M,
 Conservative
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                                                                898 A; 1210 C; 1073 G; 606 T; 0 other;
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            20.0%;
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Schmitz A, Sers
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            Score 24.6;
Pred. No. 54;
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rs C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour suppressor gene; chromosome 6q27; cancer; therapy; human; D6S297; breast cancer; ovarian cancer; lymphoid cancer; marker; D6S193; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 cactgactggt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gtactgcgtctgccggctgccctacgacgttacccgctttatgatcgagtgcgatgcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                   /*tag= o
4912..5093
                                                                                                                                                                     /*tag= n
4878..4927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= g
2749..2843
                                                                                                                                                                                                             /*tag= m
4854..4903
                                                                                                                                                                                                                                                                                                                            /*tag= j
/note= "trapped exon"
3654..3793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "putative polymorphism, pDJ84g15" complement (2310..2482)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "putative polymorphism,
    "pDJ84g15"
replace(1920,T)
                                      complement
                                                                                              complement
                                                                                                            /*tag=
                                                                                                                                                                                                                                                        complement
                                                                                                                                                                                                                                                                                          complement
                                                                                                                                                                                                                                                                                                                                                                                         complement (3083..3201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (719..724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                        /*tag= q
/note= "match:
                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                               /note= "putative polymorphism,
pDJ84g15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(2984,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  replace(1128,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1126..1220 ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "MIR repeat family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68940
                                                                                                                                                                                                                                                                                                                                                                                                             pDJ84g
                                      (5558..5607)
                                                                                              (5398..5563)
                                                                                                                                                                                                                                                        (4615..4664)
                                                                                                                                                                                                                                                                                          (4483..4532)
                                                        D6S193 microsatellite"
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/note= "putative polymorphism, pbJ84g15, G in 255h6" complement (15609..15614) /*tag= at 16174..16451
 complement (16867..16939)
/*tag= aw
/note= "trapped exon"
16867..17013
                                                                                                                                                                                                                                             /*tag= an
/note= "trapped exon"
complement (14197..14400)
                                                                                                                                                                                         /*tag= ap
/note= "L1 repeat family"
complement (14607..14860)
                                                                                                                                                                                                                            complement (14496..14601)
                                                                                                                                                                                                                                                                                                                                                                       complement (10706..10761)

/*tag= ai
/*tine=7..11368
                                                                                                                                                                                                                                                                              complement (12641..12690)
/*tag= am
13800..14074
                                                                                                                                                                                                                                                                                                             complement (12270..12275)
/*tag= al
                                                                                                                                                                                                                                                                                                                                        /*tag= aj
/note= "Alu repeat family"
11264..11315
                                                                                                                                                                                                                                                                                                                                                                                                        complement (10669..10761)
/*tag= ah
                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (9636..9685)
/*tag= af
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= ac
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complement (9467..9583)
/*tag= ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (8543..8593)
/*tag= ab
/note= "trapped exon"
9351..9678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (6887..6892)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (6395..6456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6395..6438)
/*tag= u
                                                 /noté= "Alu repeat family"
16509..16559
                                                                                                                                             replace(15091,G)
                                                                                                                                                               /note= "trapped exon"
14930..14979
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (10423..10461)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (8414..8447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (7237..7434)
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/note= "trapped exon"
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Best Local S
Matches 54
48374 tgaaaaatgacttaaagtataggtcaaatatacatgccatgcgggtgctccaagagatgg 48433
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                                                                                                                                                                          repeat_region
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                                                                                                                        repeat_region
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          Similarity
                                         Conservative
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complement (17427..17606)
/*tag= az
17647..17696
/*tag= ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tay
complement
                                                                                                                                                                         /*tag= bu
32483..32488
/*tag= bv
33639..33870
                                                                                                                                                                                                                            30550..31665

/*tag= bs

30550..30863

/*tag= bt
                                                                              complement (34638..34996)

/*tag= by
/note= "TIGGER2 repeat family"
complement (34879..34941)
/*tag= bz
                                                                                                                                        /*tag= bw
/note= "Alu repeat family"
complement (33782..33867)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= bd
/note= "MER20 repeat family"
19688..19975
                                                                                                                                                                                                                                                                                                                                                                                                                                              21450..21499
/*tag= bj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= bh
/note= "Alu repeat family"
21292..21341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "putative polymorphism complement (20770..20878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= ax
/note= "trapped exon"
17288..17352
                                                                                                                                                                                                                                                                                                   /*tag= bp
24266..24315
                                                                                                                                                                                                                                                                                                                     /note= "putative polymorphism (T)5 in pDJ84g15"
complement (24244 . 24293)
                                                                                                                                                                                                                                                                                                                                                    replace(24182..24186)
                                                                                                                                                                                                                                                                                                                                                                        complement (23288..23293)
                                                                                                                                                                                                                                                                                                                                                                                           complement (23196..23233)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        replace(20729..20767)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Alu repeat family"
20108..20226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (18367..18416)
/*tag= bb
                                                                                                                                                                                                                                                                              complement(24600..24649)
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (22392..22441)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (19301..19334)
                                                                                                                                                                                                                                                                                          /*tag= bq
                                                  20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (19541..19683)
                                       Score 24.6; DB 20;
Pred. No. 1.5e+02;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TAT13) in 52b3"
                                         Indels
                                                           Length 68940;
                                        0;
                                       Gaps
                                        0;
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repeat_region

exon

exon

exon

exon

promoter

exon exon

7..9678

exon

exon exon

..8695

exon

exon exon exon exon

/*tag= s 6072..6134

exon

polyA_site

exon

exon exon

repeat_region polyA_site

′*tag=

exon

repeat_region

exon

variation promoter exon

promoter polyA_site

F.J	FT T	T T T	FT	L'I	FT	FT	FT	FT	FT	# # # # # #	FT	FI	FT	FT	FT	13 1. 15 1.	E T	17.	FT	FT	F	111	F T F	1 H	FH.	20 XX	X X X	XX XX	X D	ž č	X II A	RES	Db	Qy
	CDS		CDS	CDS	RBS		CDS	RBS .	CDS	CDS	RBS		CDS	CDS	RBS		CDS	RBS	CDS	RBS		CDS	RBS	Č	Key	Micromonospora c	Everninomicin; au fermentation; ds	Micromonospora [26-SEP-2001 (fi	AAS08693;	ID AAS08693 standard;	ULT 43	48434 acaaattgato	74 taagtttcaca
	/note= "No start codon" complement (1210813022)	/*tag= r /product= "EvdK" /partial	-12	1042411176 /*tag= q	complement (1023210235) /*tag= p	"EvdI"	/*tag= n complement (946310224)	8 C		/2/2.832/ /*tag= 1 /product= "Rydg"	62266229 7.*tag= k	/*tag= j /product= "Evdf"	72	53096235 /*tag= i	8	/product= "EvdD"	/*Cag= I /41435312	/product= "EvdC" complement (38673870)	nent e	complement (26182622) /*tag= d	"EvdB"	3	ment	3	Location/Qualifiers	carbonacea var. africana.	<pre>antibiotic; bottle-neck gene; orthomicin; s.</pre>	DNA encoding biosynthetic enzymes for Everninomycin.	(first entry)		rd; DNA; 109519 BP.		acaaattgatcttattgatcatatttttatacctttaattaca 48476	taagtttcacatgtaaggtgatacttatcttcaatttattcca 116
																				_														
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	CDS	CDS		CDS	CDS	RBS		CDS	RBS	CDS	CDS	RBS		CDS	RBS	CDS	,	CDS	RBS	CDS	RBS	7	CDS	RBS	CEC	GD6	CDS	CDS		CDS	CDS	RBS	CDS	RBS
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        18 agatgeettacaaccetgatgacetaatggegeaatgegagggetgeactgactg
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/product= "EvsC"

53554..54207
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51629..51622
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                           Score 24.6; DB 22;
Pred. No. 1.7e+02;
0; Mismatches 19;
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                                          Length 109519;
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AAC75339/c
ID AAC75339 standard; cDNA; 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058473-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000WO-US08621
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31-MAR-1999; 02-APR-1999; 05-APR-1999; 99US-0127607. 99US-0127636. 99US-0127728.

(CURA-) CURAGEN CORP

30-MAR-2000;

2000US-0540763

RA, Leach

WPI; 2000-602362/57. P-PSDB; AAB41130.

Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease frame ×

Claim 5; Page 1399; 5507pp; English.

antiinflammatory; antibacterial; antivital; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance AAC74446 to AAC77606 encode the proteins given in AAB40237 to which represent the human ORTX open reading frames 1 to 3161. sequences have activities such as: cytostatic; hepatotropic; vantipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; coagulation; 6 inhibit thrombosis; a contraceptive to AAB43397, 51. The ORFX vulnerary;

Sequence 294 BP; 96 Α; 51 c; 8 G; 79 Ţ., 0 other;

RESULT

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RESULT 45
AAA01147/c
ID AAA01147 standard; cDNA; 300 BP.
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Best Local (
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Reinhard C, Giese K, ka
Reinhard C, Drmanac R, Cr
sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of
                                                                                                                                                                         AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test
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15-MAY-1998;
15-MAY-1998;
                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probe; detection; cancerous state; metastasis; identification;
breast cancer; oestrogen receptor-positive breast cancer; therapy;
oestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                             cells
                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP. (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                              Page 454; 1097pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer; tumour; diagnosis; gene expression product;
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98US-0085537.
98US-0085696.
98US-0105234.
98US-0105877.
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Randazzo F, Kennedy GC, I
Crkvenjakov R, Dickson M,
Garcia V, Jones LW, Stav
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states,

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responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-negative breast cancer, lung cancer, and colon cancer.
Sequence 300
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BP; 85 A; 72 C; 73 G; 70 T; 0 other;

δÃ Query Match Best Local S Matches 37 1 caggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgag Similarity Conservative 19.8%; 63.8%; 0; Score 24.4; Pred. No. 27; Mismatches DB 21; 21; Length 300; 0; 58 Gaps

CATGTATTGGAAACTTAATCTCCAATGCAACAGTGATGGGAGATGGGCCCCAATGGGAG

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Search completed: March 19, Job time: 2850 sec 2002, 10:21:41

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Result
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Maximum DB
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US-08-164-839-32
US-08-164-839-79
US-08-164-839-71
US-08-164-839-71
US-08-164-839-71
US-08-583-799-71
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US-08-152-019A-44
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US-08-253-785-2
US-08-152-019A-5
US-08-152-019A-6
US-08-253-785-2
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71 tggtaagtttcacatgtaaggtgatacttatcttcaatttattccacacaac 122
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AAATGCTTGCAATCTGACTATTAACAGCACCAATTTGCGCGCCTTGCGTGTTGCCTTGTG 4587

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18.5	18.5	18.5	18.5	18.5	18.5	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7
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Sequence 2, Appli	Sequence 81, Appl	Sequence 774, App	Sequence 5, Appli	Sequence 7, Appli	Sequence 2, Appli		Sequence 35, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli		Sequence 30, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli	Sequence 7, Appli

ALIGNMENTS

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-477-451-9
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US-08-477-451-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/08477451 Patent No. 5928865
                                 Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                TELEPAX: 510-033-13-11
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
SEQUENCE SHARACTERISTICS:
SEQUENCE SAME PAIRS
LENGTH: 5599 base pairs
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
TITLE OF INVENTION: Helicobacter
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                     TELEPHONE: 510-055-3542
mer.efaX: 510-655-3542
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ZIP: 94608-2916
                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CA
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                                                                                                                                                            nucleic acid
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4560 Horton Street
 Conservative
                                                                                                                            linear
                                                                                                         DNA (genomic)
                20.8%;
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                  Score 25.6;
Pred. No. 5
 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
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US-08-477-451-25
US-08-477-451-25
Sequence 25, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
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Patent No. 592000
PATENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         4588 CGTTAAATTCCCCTGTTAATTTGCTAATATTTAAGATATTGTTCCCCACAGC 4639
                                                                                                                       APPLICANT: Covacci, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
                                                                                                                                                                                                                                                                           1012 CGTTAAATTCCCCTGTTAATTTGCTAATATTTAAGATATTGTTCCCCACAGC 961
                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                             NUMBER OF SEQUENCES:
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                              STREET: 4500
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CITY: Emeryville
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mes 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 5599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 07-JUN
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                COUNTRY:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                         Chiron Corporation
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)N: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08390878 Patent No. 5700683
                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATTON:
 TELEFAX: 4: INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                 REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8145 CGTTAAATTCCCCCTGTTAATTTGCTAATATTTAAGATATTGTTCCCCACAGC 8196
                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stover, Charles K.
APPLICANT: Mahairas, Gregory G.
TITLE OF INVENTION: VIRULENCE-ATTENUATING GENETIC DELETIONS
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
TELEPHONE: 410/5043/5043 TD NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 aaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcactgac 70
                                                                                REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                   STREET: One M
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TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McClung, Barbara G. REGISTRATION NUMBER: 33,113 REFERENCE/DOCKET NUMBER: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 07-JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                        CITY:
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                        San Francisco
                                                                                                                                                                                                                                                                                                                                    California
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One Market Plaza, Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                    USA
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                                    415/543/9600
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07-JUN-1995
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Pred. No. 8.9;
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                                                                                                                                                                                                               Version #1.30
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SEQUENCE CHARACTERISTICS

ENGTH:

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; NAME/KEY:
; LOCATION:
US-08-741-134-1
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Best Local, Similarity 66.7
  Query Match
Best Local Similarity
Matches 55; Conserv
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                                                                                                                                                                                                                    NFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TUTELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,163
FILING DATE: 01-NOV-1995
CLASSIFICATION: 424
                                                                                                                    FEATURE:
                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect for Windows CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.11
                                                                                                                                               TOPOLOGY:
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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    Conservative
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                20.3%;
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Score 25; DB Pred. No. 6.5; 0; Mismatches
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Pred. No. 1
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              DB 5.5;
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                            Length 2255;
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  Indels
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RESULT 6
US-08-164-839-30
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                             Query Match
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                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: 1
                                                                                                                                                                                                          LENGTH: 2064 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
               Local
                                                                                                                                     TISSUE TYPE:
                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                NAME: Oblon, No. 5514573man REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, McCLELLAND, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway,
                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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(: U.S.A.
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(703)413-2220
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                                                                                                                                                Paralichthys olivaceus
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HIROSHI
               20.2%;
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                                                                                                                                                                                                                                                                                                                                                             24,618
0;
              Score 24.8;
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                    10-599-0
ed. No. 7.4;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fourth Floor
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                            DB 1;
                            Length 2064;
Indels
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Gaps
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US-08-164-839-32
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                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: YASUEL
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APPLICANT:
APPLICANT:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/01
FILING DATE: 14-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                 633
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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68 gactggtaagtttcac 83
                                                                                                                                                                                                                                    TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
STATE: Virginia
                                                                                                          Local
                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                     NAME/KEY:
                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Oblon, No. 5514573man F. REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT ADDRESSEE: P.C.
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                                                                                                                                                                                                                                                                                                                                        ENGTH:
                                                   tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTGGTCAGTGGCAC 708
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                              TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGGTGTGCT 692
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5. 5514573
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nucleic acid
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(703)413-2220
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VENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
VENTION: FROM FISH
EQUENCES: 72
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                                                                                          Conservative
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Pred. No. 7.4;
0; Mismatches 32
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US-08-583-799-30
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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GACTGGTCAGTGGCAC
                          gactggtaagtttcac 83
                                                           TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 692
                                                                                                                                    Similarity
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(703)413-2220
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                                                                                                                      Conservative
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RESULT 9 US-08-583-799-32

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US-08-583-799-32
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ORIGINAL SOURCE:
ORGANISM: Para
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/00
FILING DATE: 14-JAN-1993
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NAME: Oblon, No. 5607849
REGISTRATION NUMBER: 24,
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STATE: Virginia
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1755 Jefferson Davis Highway, Fourth Floor
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NAKANISHI, KAZUO
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                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 7.4;
); Mismatches
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Pred. No. 7
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US-08-164-839-71

US-08-164-839-71

; Sequence 71, Application US/08164839

; Patent No. 5514573

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (703)413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (703)412-3000
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                                                                                                                                                                       661 TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
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                                                                                                           721 GACTGGTCAGTGGCAC 736
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COUNTRY: U...
22202
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LOCATION:
                                                                                                                            68 gactggtaagtttcac 83
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Virginia
                                                                                                                                                                                       8 tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                 44;
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DEDNESS: double
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    P.C.
    1755 Jefferson Davis Highway, Fourth Floor

                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (703)413-2220
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26..2092
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                               Score 24.8; DB Pred. No. 7.6; 0; Mismatches
                                                                                                                                                                                                                                 0;
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Best Local Similarity 5/...
44; Conservative
                                           Patent No. 5607849 GENERAL INFORMATION:
                                                                           Sequence 69,
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ODLON, NO. 5514573man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-59
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APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
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APPLICANT:
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STATE: Virginia
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                    GACTGGTCAGTGGCAC 736
                                                                                                                                                                                gactggtaagtttcac 83
                                                                                                                                                                                                              TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 2148 base pairs
nucleic acid
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                                                                         Application US/08583799
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1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)413-2220
MOTOKI, MASAO
               NAKANISHI,
                            YASUEDA, HISASHI
                                                                                                                                                                                                                                                                                                                                                                 CDS
26..2092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA to mRNA
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                                                                                                                                                                                                                                                                                         20.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71:
                                                                                                                                                                                                                                                                         Score 24.8; DE Pred. No. 7.6; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-599-0
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US-08-583-799-69
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                                                                                                                                                        RESULT
                                                                                                          Sequence 71, Applio Patent No. 5607849
                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                               GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE: FEATURE:
                                             APPLICANT:
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ORIGINAL SOURCE:
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MEDIUM TYPE: Floppy disk
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APPLICANT: MATSUI, HIROSHI
TITLE OF INVENTION: GENE ENCODING TRANSGLUTAMINASE DERIVED
TITLE OF INVENTION: FROM FISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5607849man F.
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PRIOR APPLICATION DATA:
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                                                                             APPLICANT:
FITLE OF INVENTION:
                 APPLICANT:
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                              APPLICANT:
                                                                                                                                                                                                         721 GACTGGTCAGTGGCAC 736
                                                                                                                                                                                                                                                                      661 TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Oblon, No. 560 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/0
FILING DATE: 14-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1755 Je
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                          gactggtaagtttcac 83
                                                                                                                                                                                                                                                                                        tgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcact 67
                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Virginia
                                                                                                                         Application US/08583799
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                                             YASUEDA, HISASHI
NAKANISHI, KAZUO
MOTOKI, MASAO
                                                                                                                                                                                                                                                                                                                                    Conservative
                                NAGASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PatentIn Release #1.0, Version #1.25
                 MATSUI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paralichthys olivaceus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA to mRNA
                HIROSHI
                                  KAZUO
                                                                                                                                                                                                                                                                                                                                                 20.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPIVAK, McCLELLAND, MAIER & NEUSTADT
GENE ENCODING TRANSGLUTAMINASE DERIVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/004,729
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                                                                                                                                                                                                                                                                                                                                  Score 24.8; DB Pred. No. 7.6; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                    32;
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CORRESPONDENCE ADDRESS TITLE OF INVENTION:

OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT

NUMBER OF SEQUENCES:

FROM FISH

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; LOCATION:
US-08-583-799-71:
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                                                                                                                                                        Sequence 5, Application US/09318448 Patent No. 6210950 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                  APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                 CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
SOFTWARE: PatentIn Ver. 2.0
                  NUMBER OF SEQ ID NOS: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 2148 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Oblon, No. 5607849man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-599
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/004,729
FILING DATE: 14-JAN-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     721 GACTGGTCAGTGGCAC 736
                                                                                                                                                                                                                                                                                                                                                        661 TGTCTATGTCAGCAGGATGATCACTGCGATGGTGAACTCTAACGGTGACAGGGGTGTGCT 720
                                                                                                                                                                                                                                                                                                         68 gactggtaagtttcac 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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TELEFAX: 248855 OPAT UR
TO NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 2148 base pairs
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PatentIn Release #1.0, Version #1.25
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Pred. No. 7.
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                                                                                                    PREVENTING, AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 2148;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-318-448-5
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US-08-152-019A-44
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                                                                       US-08-152-019A-44
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LENGTH:
Matches
             Query Match
Best Local :
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                                                                                                                                                                        TELEX: 910 277299 FHT UR INFORMATION FOR SEQ ID NO: 4
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                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OSMAD, Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59012/RAO
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 781-1989
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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ADDRESSEE: FLEHR, HOHBACH,
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                                                                                      MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NEURAL AXON OUTGROWTH MODULATORS NUMBER OF SEQUENCES: 46
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                                                                                                                                                                                         TELEPHONE: (415) 398-3249
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 12-NOV-1993 CLASSIFICATION: 514
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                  TOPOLOGY:
                                                                                                              STRANDEDNESS:
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                                                                                                                                           LENGTH:
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             Similarity
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                                                                                                                            nucleic acid
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                                                                                                                                          1839 base pairs
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Jessell, Thomas
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Kennedy, Timothy
Conservative
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             Score 24.2;
Pred. No. 12;
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Mismatches
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48;
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Indels
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RESULT 17
US-08-727-034-5
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                                             Sequence 5, Application US/08727034 Patent No. 5665872 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1839 base pairs
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/482,677
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 14
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                                                                                                                                                                                                                                                                                                                                176 CTGTTATTGCTAGTGATACATGCGGAACAAACCGACCAGACAAGTATTGTACTGTGAAGG 235
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                                                                                                                                                                                                                                236 AGGGTCCGGATGGAATTATCCGTGAGCAATGTGACACTTGT 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
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Similarity 52.5%;
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Kennedy, Timothy
Placzek, Marysia
Jessel, Thomas
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SAITO, YASHUSI
IWASAKI, AKIO
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                          YASHUSHI
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Pred. No. 12;
0; Mismatches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                             GENERAL INFORMATION:
APPLICANT: SALTO, YASHUSHI
APPLICANT: IMASAKI, AKIO
APPLICANT: ARAI, KOICHI
APPLICANT: YAMAZAKI, HIROY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 261440/1995
APPLICATION NUMBER: JP 261440/1995
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APPLICATION NUMBER: JP 261440
                                                  CORRESPONDENCE ADDRESS
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APPLICATION NUMBER:
FILING DATE: 24-APR-
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ADDRESSEE: P.C.
ADDRESSEE: P.C.
ADDRESSEE: P.C.
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 S. CITY: ARLINGTON
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                        ADDRESSEE:
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SYSTEM: PC-DOS/MS-DOS
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52.5%;
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Pred. No. 19;
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APPLICANT: ARAI, KOICHI
APPLICANT: YAMAZAKI, HIROYUKI
TITLE OF INVENTION: NOVEL LDL RECEPTOR ANALOG
TITLE OF INVENTION: THE GENE CODING THEREFOR
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5248 CCACCAGATATCCACATTGACAGCTATGGTGAAAATTATCT
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CORRESPONDENCE ADDRESS:
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OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
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; NAME/KEY: misc_feature
; LOCATION: 165..6722
; OTHER INFORMATION: Cfunc
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US-08-727-034-6
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                                                                 Sequence 2, Application US/08253785 Patent No. 5633363
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Best Local S
                                                GENERAL INFORMATION:
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                                                                                                                                                               5328 CCACCAGATATCCACATTGACAGCTATGGTGAAAATTATCT 5368
                                                                                                                                                                                                                              5268 GGAATAGGAAACTGGAGCGATTCTAAAATCCATTACCACCATAAAAGGAAAAGTGATCCCA 5327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 10
FILING DATE: 24-APR-1996
ATTORNEY/AGENT INFORMATION:
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                  APPLICANT:
                                 APPLICANT:
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     APPLICANT:
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OPERATING SYSTEM: F
SOFTWARE: PatentIn
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LOCATION:
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REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: sig_peptide LOCATION: 81..164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                              53,
                                                                                                                                                                                                                                                                                                           Similarity
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81..6725
Colbert, James T. Held, Bruce M. Wurtele, Eve S.
                                                                                                                                                                                                                                                                                            Conservative
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SYSTEM: PC-DOS/MS-DOS
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09-OCT-1995
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24-APR-1996
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encode the mature peptide"
/note= "Identification Method: S"
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Pred. No. 19;
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US-08-975-316-53/c
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Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415/857-1125 INFORMATION FOR SEQ ID NO:
                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1001 TAAATCTTCCATGCCTTGGAACCCATATGACATTGTGGCCTTATTTGATTCATACTCACC 942
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                         APPLICANT:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                COMPUTER:
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LOCATION: 51..185
OTHER INFORMATION:
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                                                                                                                                            STREET:
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STRANDEDNESS: single
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                                            MEDIUM TYPE:
                                                                                                               STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                          Seattle
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                                                                                                                                            2601 Elliott Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2329 base pairs
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                IBM Compatible SYSTEM: DOS
                                                                                              USA
                                                                                                                                                                                                        BLOKSBERG, Leonard N., HAVUKKALA, Ilkka
and GRIERSON, Alastair W.
VENTION: MATERIALS AND METHODS FOR
VENTION: THE MODIFICATION OF PLANT LIGNIN CONTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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FastSEQ for Windows Version 2.0
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Pred. No. 21;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/975,316

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                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION UNMER: 37,007
REFERENCE/DOCKET NUMBER: 1100
TELECOMMUNICATION INFORMATION:
TELEFAX: 206-20 INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/713,000
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grierson, Alastair
TITLE OF INVENTION: MATERIALS AND METHODS FOR THE
TITLE OF INVENTION: MODIFICATION OF PLANT LIGNIN C
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
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                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
                            TELEPHONE:
                                                                                                                                                                                                               MEDIUM TYPE:
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              206-269-0563
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01 Elliott Avenue, Suite 4185
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BER: 11000/1003C1
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Pred. No. 15;
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Matches

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                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1026 base pairs
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: September 1
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BLOKSBERG, Leonard N., HAVUKKALA, APPLICANT: and GRIERSON, Alastair W. TITLE OF INVENTION: MATERIALS AND METHODS FOR TITLE OF INVENTION: THE MODIFICATION OF PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
Local Similarity
les 42; Conserv
                                                                                                                            LENGTH:
                                                                                                                                                                           TELEX:
                                                                                                                                                                                                                                                NAME: SLEATH, Janet REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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linear
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            Score 23.4;
Pred. No. 19;
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suite 4185
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                            DB 2;
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                         Length 1026;
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us-09-211-710-6/c

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; OTHER INFORMATION: beta-cyclase
US-09-201-641-1
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Best Local Similarity
Thes 42; Conserv
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; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-211-710-6
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APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
APPLICANT: Grierson, Alastair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cunningham Jr, Francis X
APPLICANT: Dellatenna, Dean
TITLE OF INVENTION: Method for Regulating Carotenoid Biosynthesis
TITLE OF INVENTION: Marigolds
FILE REFERENCE: Quest 41-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 11000.103c3
CURRENT APPLICATION NUMBER: US/09/211,710A
CURRENT FILING DATE: 1998-12-14
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/201,641A CURRENT FILING DATE: 1998-11-30
                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Materials and Methods for the TITLE OF INVENTION: Modification of Plant Lignin
                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Tagetes erecta
FEATURE:
NAME/KEY: CDS
                                                                                                                                                                                                                                                                             LENGTH: 1959
1005 tcaatatgataagccttataaccctgggtaccaagtggc 1043
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                   10 taaatgtgagatgccttacaaccctgatgacctaatggc 48
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                                                                       Conservative
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Pred. No. 19;
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US-08-244-686-1
                                                                                                                                                                      US-08-244-686-1
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                                                                                           Matches
                                                                                                         Query Match
Best Local :
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                 1322 ATTGGGAGATGCGGGGTGCTGCGTACGCTCTAAGGTAGGGCATTTAAAGGGATATTTAGC 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Aspergillus niger var. awamori
STRAIN: CBS 115.52 (ATCC 11358)
IMMEDIATE SOURCE:
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LOCATION: 581..629
LDENTIFICATION METHOD:
OTHER INFORMATION: /evi
                                                   43 aatggcgcaatgcgagggctgcactgactggtaagtttcacatgtaaggtgatacttatc 102
                                                                                         Local Similarity 55.7 nes 44; Conservative
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OTHER INFORMATION:
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IDENTIFICATION METHOD:
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ttcaatttattccacacaa 121
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ucleic acid
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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join(432..5
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351..431
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55.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Process for the production of a protein using endoxylanase II (exlA) expression signals
                                                                                                                                                                                                  D: experimental.
FEC_number= 3.2.1.8
/product= 'pre-pro endoxylanase
/evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                             /EC_number= 3.2.1.8
/product= "endoxylanase
/evidence= EXPERIMENTAL
                                                                                                                                                                                     /gene= "exlA"
                                                                                                                                                                                                                                                                                                               /gene= "exlA"
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/evidence= EXPER
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                                                                                           Score 23; DB Pred. No. 34; 0; Mismatches
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                                                                                                                        Length 2059;
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RESULT 27
US-08-852-091-7/c
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US-08-369-796-7
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US-08-369-796-7/c
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             Sequence 7, Application US/08852091 Patent No. 5883228
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                                                                                                                                                               Matches
                                                                                                                                                                           Query Match
Best Local Similarity
GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pair:
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TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: cD
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 06-JAN-1995 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ORGANISM: Mou
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                                                                                                      538 CTGAGAGGTTTTGCATTTAAAGTCATATTCATCTTGTAATTCTTCTA 492
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     70 ctggtaagtttcacatgtaaggtgatacttatcttcaatttattcca 116
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TELEPHONE: ZU1
TELEPHONE: ZU1
TELEPHONE: ZU1
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                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Hackensack
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 INFORMATION:
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                                                                                                                                                                           Score 23;
Pred. No.
                                                                                                                                                               Mismatches
                                                                                                                                                                           DB 1;
35;
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                                                                                                                                                                                          Length 2277;
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                                                                                                                                  RESULT 28
US-08-820-754-7/c
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TITLE
                           APPLICANT:
                                            APPLICANT:
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               APPLICANT:
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Sequence 7, Application US/08820754 Patent No. 5976835
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Best Local Similarity
                                                                                   GENERAL INFORMATION:
APPLICANT: Darnel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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PRIOR APPLICATION DATA:
08/369,796
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LENGTH: 2277 base pairs
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ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
   CLONE: Murine Stat91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
INVENTION:
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                                                               Darnell Jr., James E. Schindler, Christian W.
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Curt M. Ho
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                               Wen, Zilong
                                                   Fu, Xian-Yuan
                 Zhong, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse
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68.1%;
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 RECEPTOR RECOGNITION FACTORS, PROTEIN
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Pred. No.
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US-08-956-652-7/c

; Sequence 7, Application US/08956652

; Patent No. 6013475
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GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/126,588
FILING DATE: 24-SEP-1993
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LENGTH: 2277 base pairs
                                                                                                                                                                                                                                                                                                         FEATURE:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: WO US93/02569
FILING DATE: 19-MAR-1993
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APPLICATION NUMBER: US 08/212,185
FILING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NORMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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TELEPHONE: 201 487-5800
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TELEFAX: 133521
                                                                                                           538 CTGAGAGGTTTTGCATTTAAAGTCATATTCATCTTGTAATTCTTCTA 492
                                                                                                                               70 ctggtaagtttcacatgtaaggtgatacttatcttcaatttattcca 116
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                        CLONE: Murine Stat91
                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 600
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STATE: New Jerse
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ER: 600-1-073 CIP
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Pred. No.
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US-08-956-652-7
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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NUMBER OF SEQUENCES:
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                                                                             Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
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411 Hackensack Avenue
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UMBER: US 07/980,498
23-NOV-1992
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68.1%;
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                                                           Score 23; DB 3; Length 2277; Pred. No. 35; o; Mismatches 15; Indels
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US-08-956-869-7
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              Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                        FEATURE:
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ORGANISM: Mouse
IMMEDIATE SOURCE:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                          MOLECULE TYPE: CI
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ATTORNEY/AGENT INFORMATION:
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TOPOLOGY: unl
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STATE: New Jersey
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                                                                                                                                                                                                                                                                                     LENGTH: 2277 base pairs
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Fu, Xian-Yuan
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              Score 23; DB 3; Length 2277; Pred. No. 35;
Mismatches
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LOCATION:
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                                                             ORGANISM: Mouse IMMEDIATE SOURCE: CLONE: Murine Stat91
                                FEATURE:
NAME/KEY:
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TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: WO US
FILING DATE: 19-MAR-1993
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ADDRESSEE: Klauber & Jackson
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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FILING DATE: 11-MAR-1994
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24-SEP-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECEPTOR RECOGNITION FACTORS, PROTEIN SEQUENCES AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/854,296
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Best Local Similarity
Matches 32; Conserv
               Query Match
Best Local Similarity
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      Matches
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                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REGESTRATION NUMBER: 600 TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/369,796
FILING DATE: 06-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17025
                                                                                                                                                    ORIGINAL SOURCE:
ORGANISM: MOUS
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
                                                                                                                         FEATURE:
                                                                                                                                                                                                HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: James E. Darnell, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    538 CTGAGAGGTTTTGCATTTAAAGTCATATTCATCTTGTAATTCTTCTA 492
                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                      CLONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: (ZIP: 0760)
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    Conservative
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 Score 23; DB 5;
Pred. No. 35;
0; Mismatches 1
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US-09-318-448-30
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Best Local Similarity
Watches 47; Conserva
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APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
                                                                                                                                            Best
                                                                                                                                                                                                                                                                                        SEQ ID NO 27
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                                                                                                                       Matches
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Patent No. 6210950
                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR TITLE OF INVENTION: PROCESSING FILE REPERENCE: 233/221 CURRENT APPLICATION NUMBER: US/09/056,105 CURRENT FILING DATE: 1998-04-06 EARLIER APPLICATION NUMBER: 60/043,467 EARLIER FILING DATE: 1997-04-10
                                                                                                                                                                                                                                                LENGTH: 42
TYPE: DNA
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KIPPS, THO
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CURRENT FILING DATE: 199-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
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                                                 2910 ttgaaaatgactgctaccttatatccccttctcaccttaggcctctcttctgtggaaactc 2969
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               67
                                                                                                                         Local Similarity 60. nes 38; Conservative
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                                                                    7 ttgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctgcac
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tga 69
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                                                                                                                                          18.7%;
60.3%;
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                                                                                                                     Score 23; DB 4; Length 4233; Pred. No. 45; 0; Mismatches 25; Indels
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Pred. No. 41;
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2970 tga 2972

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; LENGTH: 4440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-1
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US-07-792-600-1/c
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                                                                          SEQ ID NO 1
                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09157021A Patent No. 6100023
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Best Local
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                                                                                                         CURRENT APPLICATION NUMBER: US/09/157,021A CURRENT FILING DATE: 1998-09-18 EARLIER APPLICATION NUMBER: 07/792,600 EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35
                                                                                          SOFTWARE:
                                                                                                                                                                                                  APPLICANT: Copeland, william C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Design Assay FILE REFERENCE: STDU-03484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER 6.
REGISTRATION UNMER: 32,837
REFERENCE/DOCKET NUMBER: STDU
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
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                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: TEMPLATE-DEPENDENT ENZYMATIC SYNTHESIS OF NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: COPELAND, WILLIAM APPLICANT: WANG, TERESA S.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 199111 CLASSIFICATION: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: NUCLEIC STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.7%;
1 Similarity 68.1%;
32; Conservation
                                                                                          PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35
; LENGTH: 5433
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-157-021-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: Homo sapiens US-09-156-842-1
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                                                              Query Match
Best Local Similarity
Matches 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09156842A Patent No. 6103473
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Design Assay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/156,842A CURRENT FILING DATE: 1998-09-18 EARLIER APPLICATION NUMBER: 07/792,600 EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/157,021A CURRENT FILING DATE: 1998-09-18
                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: 07/792,600 EARLIER FILING DATE: 1991-11-15 NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Copeland, William C. APPLICANT: Wang, Teresa S. F. TITLE OF INVENTION: Drug Screen FILE REFERENCE: STDU-03485
                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: STDU-03484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 4440
 408 GGTTTTGTCACTGCGAGCTTCTTTACATTCCTCTTGTCTTTATTGCG 362
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                 ggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcg 49
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Similarity 68.1%;
                                                                Conservative
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68.1%;
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                                                              Score 23; DB Pred. No. 49; 0; Mismatches
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                                                                                             Length 5433;
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RESULT 40
US-08-483-503A-2
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; ORGANISM: Homo sapiens
US-09-156-842-35
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Patent No. 6017880
GENERAL INFORMATTY
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NUMBER OF SEQ ID NOS: 35
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                                                                                                                                                                                                                                        APPLICATION NUMBER: US
FILING DATE: 07-JUN-19
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5433
                                                                                                                           APPLICATION NUMBER: US 08/209,040
FILING DATE: 09-WAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,369
FILING DATE: 09-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-3315
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STREET: 1300 I Street, N.W.
                                 TELEPHONE:
                                                                         REFERENCE/DOCKET NUMBER:
                                                                                           NAME: Barker, M. Paul
REGISTRATION NUMBER:
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                   202-408-4400
                                   202-408-4000
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US-08-896-605A-7/c
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GENERAL INFORMATION
GENERAL INFORMATION
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                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 1:
FILING DATE: 30-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patent In Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TANIMOTO, APPLICANT: KURIMOTO, TITLE OF INVENTION:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18 July PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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LENGTH: 180 base pairs
                                                                                       FEATURE:
                                                                                                   MOLECULE TYPE:
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               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 19-JU
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                                                                                                                                                                                                                                                         NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08 FILING DATE: 18 July 1997
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                                                                                                                  TOPOLOGY:
                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                      NAME/KEY:
                                          IDENTIFICATION METHOD:
                                                          COCATION:
                                                                                                                                                         LENGTH:
DENTIFICATION METHOD:
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                                                                                                                                                      579 base pairs
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419 Seventh Street, N.W., Suite 300
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                                                                                                                                                                                                      202-737-3528
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SYSTEM: PC-DOS/MS-DOS
                                                          leader peptide 1..108
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                                                                                                   cDNA to mRNA
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                : peptide
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Pred No. 16;
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US-08-896-501A-5
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Best Local Similarity 50.0
    Matches
                              Query Match
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TANIMOLO, ALLA APPLICANT: KURIMOTO, Masashi
APPLICANT: KURIMOTO, MASAShi
PROCESS FOR PRODUCING POLYPEPTIDE
                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TATELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 25-JUL-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 579 base pairs
                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION NUMBER: JP 213,267/1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS
                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                       TELEPHONE: 202-737-3528
                 Local
                                                                                                         IDENTIFICATION METHOD: NAME/KEY: mat peptide LOCATION: 109..579
                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 1
                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: JP 31,474/1997 FILING DATE: 31-JAN-1997
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                                                                                                                                                                  NAME/KEY:
                                                                                         [DENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTCATTCAAATTTCTTATGACTGATAATTTAGATTCAAGCTTGCCAAAGTAATCTGATT 101
    l Similarity 50.0
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20004
                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                            BROWDY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.C.
                                                                                                                                                                                                                                                        579 base pairs
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419 Seventh Street, N.W., Suite 300
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                                                                                                                                                    leader peptide 1..108
                                                                                                                                                                                                                linear
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                                                                                                                                                                                                 cDNA to mRNA
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               18.5%;
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Score 22.8; D
Pred. No. 25;
0; Mismatches
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Pred. No. 2
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                              DB 2; Length 579;
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; FEATURE:

NAME/KEY: misc_feature

; LOCATION: (1)...(680)

; OTHER INFORMATION: n = A,T,C

US-09-328-111-774
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                                                                                                     Sequence 81, Application US/08943731
Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 774 LENGTH: 680
                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: US 60/088,801 EARLIER FILING DATE: 1998-06-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lewis, Marcia E. APPLICANT: Monahan, John E. APPLICANT: Schlegel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Catino, Theodore J
APPLICANT: Derti, Adnan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Burgess, Christopher C. APPLICANT: Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Steinmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                      APPLICANT:
APPLICANT:
                   APPLICANT:
                                    APPLICANT:
                                                                                                                                                                                                               280 gctctacgtgaagtgttatcttttttttctaagtgaca
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                                                                                                                                                                                                                                                                                                    26 tacaaccetgatgacetaatggegeaatgegagggetgeactgactggtaagtttcacat 85
                                                                                                                                                                                                                                               86 gtaaggtgatacttatcttcaatttattccacacaaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 gcactgactggtaagtttcacatgtaaggtgatacttatcttcaatttattcca 116
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SEREDA, LARISA
LARSON, ANDREA W.
                                                      SPOTILA,
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                    DELTAS,
                                                                      PROCKOP, DARWIN J.
                                      CONSTANTINOS
                                                                                                                                                                                                                                                                                                                                                                      18.5%;
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                                                        LORETTA D.
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Pred. No. 27;
0; Mismatches
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APPLICANT: APPLICANT:

COLIGE, ALAIN EARLY, JAMES

PACK, MICHAEL

APPLICANT

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                                                                                                                                                                                                                                                             Sequence 2, Application US/08884324 Patent No. 6060283
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 911 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILIG DATE: 14-MAR-1994
FILIG DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
PAPELICATION NUMBER: US 07/803,628
FILLING DATE: 03-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: DOYLE LEARY Ph.D., KATHRYN
                                                                                                                                               TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-
                                                                                                                                                                                APPLICANT: Takanori OKURA
APPLICANT: Kakuji TORIGOE
APPLICANT: Masahi KURIMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/943,731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ANDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES NUMBER OF SEQUENCES: 666
                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      774 CACTAGCTGGGAAGTGTGAAAAGAGTTCTGAAATTTTTCTTCTATTTTT 725
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STREET: FLR.
CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                         64 cactgactggtaagtttcacatgtaaggtgatacttatcttcaatttatt 113
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                                        STATE:
                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 03-OC CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
               COUNTRY:
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                                                                                            ADDRESSEE:
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20004
                                                     Washington
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                                  D.C.
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                                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W.,
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Pred. No. 30;
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                                                                        Suite 300
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Search completed: March 19, 2002, 09:58:41 Job time: 1615 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 185
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO ORIGINAL SOURCE:
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                                                                                                                                 337
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                                                                       277 CCAGGTTTTCATCATCTTCAGCTATAAAGTAAAGCGTATTGTCAATAAATTTCA 224
                                                                                                                                                                                          Local Similarity hes 57; Conserv
                                                                                        63 gcactgactggtaagtttcacatgtaaggtgatactttatcttcaatttattcca 116
                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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TISSUE TYPE:
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                                                                                                                                                  3 ggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggct 62
                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
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                                                                                                                                GGTCATTCAAATTTCTTATGACTGATAATTTAGATTCAAGCTTGCCAAAGTAATCTGATT
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286.
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178..285
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                                                                                                                                                                                                        Score 22.8;
Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OKURA=1
                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                     Length 1120;
                                                                                                                                                                                          Indels
                                                                                                                                                                                          0
                                                                                                                                                                                        Gaps
```

278

0;

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pir2: T3866
pir1: S48729
pir2: H72647
pir2: T42756
pir2: T36971
pir2: T36971
pir2: T3693
pir2: A31788
pir2: B86073
pir2: H86073
pir2: H70109
pir2: T16487
pir2: T16497
pir2: T16497
pir2: T38168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pir2:T40419
pir2:T41449
pir2:T21433
pir2:T21430
pir2:T21430
pir2:T03455
pir2:T03454
pir2:T03454
pir2:T03454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pir2:S44281
pir2:T06070
pir2:H85462
pir2:S69047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database sequences: 219241
Database length: 76174552
Search time (sec): 37.240000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query length:
Database: PIR_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of: US-09-684-016-48411 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-016-48411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           information block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9:32
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341.52
141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESCOTE | 2.5e-11 | 2.5e-11 | 2.5e-10 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09 | 2.3e-09
out_format :
                                                                                                                        receptor like protein (partial)
receptor like protein - Arabidc
ES43 protein - barley
ES43 protein | barley
ES43 protein | fimported] -
hypothetical protein F26H11.3a
hypothetical protein F26H11.3a
hypothetical protein F26H11.3a
hypothetical protein F26H11.3b
hypothetical protein F26H11.3b
ALR protein - human
l ALR protein - human
l ALR protein - human
l ALR protein - human
l ALR protein - human
l ALR protein - human
l ALR protein - human
l Appothetical protein T32A16.30
probable molybdopterin-guanine
l probable transcription regulat
glucokinase regulator - Africar
hypothetical protein F15E6.1
l Typothetical protein F15E6.1
l Typothetical protein F15E6.1
l Typothetical protein MAPE614
l Typothetical protein MAPE614
l Typothetical protein SPC645.3
l Typothetical protein SPC645.3
l Typothetical protein F5EF10.2
l Typothetical protein F5EF10.2
l Typothetical protein F5EF10.2
l Typothetical protein F5EF10.2
l Probable sucrose synthase (EC 2
l Typothetical protein SPAC2EE12.
l Typothetical protein SPAC2EE12.
l Typothetical protein SPAC2EE12.
l Typothetical protein SPAC2EE12.
l Typothetical protein SPAC2EE12.
l Typothetical protein SPAC3AB.4
l anaerobic dimethylsulfoxide red
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Documentation
                                            hypothetical protein dmsB [impo
hypothetical protein F32D8.3
hypothetical protein T5C23.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pir2:H86457
pir2:T15670
pir2:S22412
pir2:S61299
                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir2:B81869
                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                            Quality:
```

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seq_documentation_block:
    receptor like protein - Arabidopsis thaliana (fragment)
    N;Alternate names: protein AT4922140
    C;Species: Arabidopsis thaliana (mouse-ear cress)
    C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
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    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
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    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    C;Date: 02-Jun-2000 #text_change 02-Jun-2000
    A;Paccession: 749121
    A;Cacession: 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor like protein (partial) [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001 C;Accession: C85253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-201 <S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A85001; A; Accession: C85253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana A;Reference number: A85001; MUID:20083488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:T49121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: AT4g22140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: pir2:C85253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: C85253 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-684-016-48411 x C85253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 sGluGlyCysLysAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:NC_001268; NID:g7269059; PIDN:CAB79169.1; GSPDB:GN00140
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6.273
95.652
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Gaps: 0
Percent Identity: 91.304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111.
105.
117.
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52
83
75
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. 29
. 42
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i hypothetical protein C27H5
i signal peptidase (EC 3.4.99
i lipopolysaccharide heptosylt
i lipopolysaccharide heptosylt
                                                                                                                                                                                                                                                                                                                                                                                                                         H.W.; Rudd, S.; Lemcke,
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Ratio:

138.00 6.273 95.652

Percent Identity:

Length:

23 0 91.304

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A;Gene: ATSP:F19H22.200
A;Map position: 4
A;Introns: 25/1; 140/2; 163/2
                                                                                                                                                                             A;Cross-references: EMBL:AL035679; GSPDB:GN00062; ATSP:F19H22.200 A;Experimental source: cultivar Columbia; BAC clone F19H22 C;Genetics:
                                                                                                                                                                                                                                                                                        R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15184
A;Accession: T06070
A;Accession: T06070
                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ES43 protein homolog F19H22.200 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06070
                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-258 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-684-016-48411 x S44281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, February 1994 A; Reference number: $44281 A; Accession: $44281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ES43 protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-227 <SPE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S44281
R; Speulman, E.; Salamini, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:T06070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-684-016-48411 x T49121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X77575; NID:g482918; PID:g1345528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: pir2:S44281
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: S44281 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 TyrCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sGluGluCysSerAspTrp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                       Quality:
  Ratio:
124.00
5.636
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6.048
91.304
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82.609
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alignment_scores:
Quality:
Ratio:
                                                                   A; Molecule type: DNA
A; Residues: 1-353 <HAL>
                                                                                                                  A; Description: The sequence
A; Reference number: S69040
A; Accession: S69047
                                                                                                                                                                  submitted to the EMBL Data Library, December 1995 A; Description: The sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                     C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999
C;Accession: S69047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: H85462
R;anonymous, The European Union Arabidopsis Genome Sequencing
Nature 402, 769-777, 1999
C;Genetics:
A;Gene: MIPS:YPL138c
                                            A;Cross-references: EMBL:U43703; NID:g1244769; PID:g1244777; GSPDB:GN00016; MIPS:YPL1
                                                                                                                                                                                                                    R; Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms,
                                                                                                                                                                                                                                                                                                                     hypothetical protein YPL138c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:S69047
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A: Map position: 4
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A;Molecule type: DNA
A;Residues: 1-258 <STO>
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seq_documentation_block:
ES43 like protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:H85462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 PheCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy 157
                                                                                                                                                                                                                                                                                                                                                                                                                                        157 sGluGluCysSerGluTrp 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGAGGGCTGCACTGACTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:NC_001268; NID:g7270893; PIDN:CAB80573.1; GSPDB:GN00140
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5.636
95.652
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6
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                                                                                                                                                                       XVI left arm
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ф

position: 16L

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probable phd finger transcription regulator - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
C;Accession: T41449
R;RRieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21994
A;Accession: T41449
A;Accession: T41449
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-424 KRIE>
A;Cross-references: EMBL:AL031523; PIDN:CAA20664.1; GSPDB:GN00068; SPDB:SPCC594.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mlo2 protein - fission yeast (Schizosaccharomyces pombe)
(;Speciles: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40419
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D. submitted to the EMBL Data Library, October 1999
A;Reference number: Z21927
A;Accession: T40419
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US-09-684-016-48411 x T40419
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A;Experimental source: strain 972h-; cosmid c4
C;Genetics:
                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                       seq_name: pir2:T41449
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A;Map position: 2
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A; Residues: 1-329 < MC
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US-09-684-016-48411 x S69047
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                                                                                                                                                                                                                                                                                                                                                                                                     137 rMetPheGlnCysIleLeuCysGluAspTrp 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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Ratio:
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4.367
55.556
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4.156
69.565
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Gaps: 1
Percent Identity: 47.826
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44.444
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seq_documentation_block:
hypothetical protein F36H11.3c - Caenorhabditis elegans
c;Species: Caenorhabditis elegans
c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map.position: 2
A;Introns: 11/1; 42/3; 183/2; 243/2; 287/1
C;Superfamily: bromodomain homology
F;266-321/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, November 1996 A;Reference number: 219421 A;Accession: T21433
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                                   seq_name: pir2:T21435
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A; Residues: 1-405 <WIL>
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hypothetical protein F26H11.3a - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone F26H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z81515; PIDN:CAB04198.1; GSPDB:GN00020; CESP:F26H11.3a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SPDB:SPCC594.05c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain 972h-; cosmid c594
                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T21433 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-016-48411 x T21433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T41449 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-684-016-48411 x T41449
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                                                                                                                                                                                                   188 sAspSerCysGlnGlyTrp
                                                                                                                                                                                                                                                                                              172 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||:::|||||| || ||||| 133 uGlyCysAspGlyCysGluAspTrp 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 TyrCysIleCysGln......LysProAspAspGlySerTrpMetLe 133
                                                                                                                                                                                                                                                 55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 GCAATGCGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                               5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGAC.....CTAATGGC 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.00
4.429
60.870
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4.167
60.000
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Gaps:
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Gaps:
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0
34.783
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2
48.000
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A;Map position: 2
A;Introns: 116/1; 147/3; 288/2; 348/2; 392/1
C;Superfamily: bromodomain homology
F;371-426/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
hypothetical protein F78H11.3b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T21430
                                                                                                                            alignment_block:
US-09-684-016-48411 x T21430
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A;Introns: 58/1; 89/3; 230/2; 290/2; 334/1
C;Superfamily: bromodomain homology
F;313-368/Domain: bromodomain homology <BRO>
                                                                                                                                                                                                                                                              alignment_scores
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z81515; PIDN:CAB04195.1; GSPDB:GN00020; CESP:F26H11.3b
A;Experimental source: clone F26H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-510 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z19421
A;Accession: T21430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, November 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Barlow,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:T21430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reference number: Z19421
A;Accession: T21435
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: CESP:F26H11.3c
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A; Residues: 1-452 <WIL>
                                                                                      Align seg 1/1
                                                                                                                                                                                                Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 CGAGGGCTGCACTGACTGG 73
                      5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCGCAATG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy 293
                                                                                                                                                                                                                     Quality:
Ratio:
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                                                                                      to: T21430 from: 1
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4.429
60.870
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4.429
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to:
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Gaps:
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0
34.783
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0
34.783
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A;Map position: 12
C;Superfamily: human ALR protein
C;Keywords: alternative splicing
                                               alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated A;Molecule type: mRNA A;Residues: 1-5262 <PRA>
                                                                                                                                                                                                                                                                                                                                                                                  R;Prasad, R.; Zhadanov, A.B.; Sedkov, Y.; Bullrich, F.; Oncogene 15, 549-560, 1997
A;Title: Structure and expression pattern of human ALR, A;Reference number: Z14954; MUID:97388474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03454
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C; Superfamily: human ALR protein
C; Keywords: alternative splicing
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A;Title: Structure and expression pattern of human ALR, a novel gene with strong homo A;Reference number: Z14954; MUID:97388474
A;Accession: T03455
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US-09-684-016-48411 x T03455
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A;Molecule type: mRNA
A;Residues: 1-4957 <PRA>
                                                                                                                                                                                                                   A; Gene: ALR
                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:AF010403; NID:g2358284; PIDN:AAC51734.1; PID:g2358285
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: ALR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF010404; NID:g2358286; PIDN:AAC51735.1; PID:g2358287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: T03455
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    Percent Similarity:
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946 sGluArgTrp 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930 CysHisAlaProTyrValGluGluAspLeuLeuIleGlnCysArgHisCy 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 sAspSerCysGlnGlyTrp 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 CACTGACTGG 73
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    human

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                           Ratio:
60.00
4.615
65.000
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4.615
65.000
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    Percent Identity:
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                                                 Length:
                             Gaps:
    45.000
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0
45.000
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                                                                                                                                                                                                                                                                                                                                                                                                                a novel
                                                                                                                                                                                                                                                                                                                                                                                                                gene with strong homo
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seq_documentation_block:
hypothetical protein T32A16.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Oct-1999
C;Accession: T08905
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H
submitted to the protein Sequence Database, May 1999
A;Reference number: Z16518
A;Accession: T08905
A;Molecule type: DNA
A;Residues: 1-443 <BEV>
A;Cross-references: EMBL:AL078468; GSPDB:GN00062; ATSP:T32A16.30
A;Experimental source: cultivar Columbia; BAC clone T32A16
C;Genetics:
A;Gene: ATSP:T32A16.30
A;Map position: 4
A;Introns: 28/3; 81/3; 172/3
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C:Date: 15-Oct-1999 #sequence_revision 15-O
C:Accession: T25101
R:McMurray, A.
submitted to the EMBL Data Library, June 19
A:Reference number: Z19982
A:Accession: T25101
A:Status: preliminary; translated from GB/E
A:Molecule type: DNA
A:Residues: 1-416 <WILL>
A:Crossion: T416 <WILL>

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US-09-684-016-48411 x T25101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein T22C1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Specie: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
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US-09-684-016-48411 x T03454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: T03454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 CACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uLeuLeuGlnCysGluIleCysGluAspTrp 223
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3.719
59.259
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Percent Identity: 37.037
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SPDB:SPAC343.11c
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seq_documentation_block:
probable transcription regulator protein - fission
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C;Accession: T38660
                                                                                                               R;Murphy, L.; Harris, D.; Wood, V.;
submitted to the EMBL Data Library,
A;Reference number; Z21804
A;Accession: T38660
                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1588 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491
A;Reference number: A81775; MUID:20222556
A;Accession: B81911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: B81911
R;Parkhill, J; Achtman, M.; James, Holroyd, S.; Jagels, K.; Leather, Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable molybdopterin-guanine dinucleotide biosynthesis protein A NMA1417 [imported] C;Species: Neisseria meningitidis C;Species: 05-May-2000 #text_change 02-Feb-2001
A; Experimental source: strain 972h-; cosmid c343
                     A; Residues: 1-1588 <MUR>
A; Cross-references: EMBL:AL109739; NID:e1534774; PIDN:CAB52274.1; GSPDB:GN00066; SPDB
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A;Experimental source: serogroup A, strain Z2491
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A; Residues: 1-192 < PAR>
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US-09-684-016-48411 x T08905
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                                                                                                                                                                                                                                                                                                                                                                                                                                        14 TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAG
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Gaps: 2
Percent Identity: 44.828
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S.; Moule, S.; Mungall, K.; Quail, M.A.;
                                                                                                                                                            August
                                                                                                                                                              Rajandream,
August 1997
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: 66.667
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                                                                                                                                                                                    Barrell,
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Rajandre
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pombe)

A; Map position:

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hypothetical protein APE0614 - Aeropyrum pernix (strain K1) C:Species: Aeropyrum pernix C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_ch:C:Accession: H72647
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    glucokinase regulator - African clawed frog
glucokinase regulator - African clawed frog
C.Species: Xenopus laevis (African clawed frog)
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S48729; S49339
                                                                                                                R; Kawarabayasi, Y.; Hino, Y.; awa, H.; Takamiya, M.; Masuda, DNA Res. 6, 83-101, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Cloning and expression of a Xenopus liver cDNA encoding a fructose-phosphate-in A;Reference number: S48729; MUID:95010134
A;Accession: S48729
                                            A; Reference number: A72450; A; Accession: H72647
                                                                    A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy. A; Reference number: A72450; MUID:99310339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-684-016-4
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A;Residues: 1-619 <VEI>
A;Cross_references: EMBL:X80901; NID:g556677; PIDN:CAA56863.1; PID:g556678
A; Molecule type:
                          A;Status: preliminary
                                                                                                                                                                                                                                                                                       seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Veiga-da-Cunha, M.; Detheux, M.; Watelet, N.; van Eur. J. Biochem. 225, 43-51, 1994
                                                                                                                                                                                                                                                                                                                                 seq_name: pir2:H72647
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                                                                                                                                                                                                                                                                                                                                                                                                                              CAATGCGAGGGCTGCACTGACTGGTAAGTTTCAC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTATTGTAAAT . . . GTGAGATGCCTTACAACCCTGATGACCTAATGGCG
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                                                                                                                                                                                                                                                                                                                                                                                  gAspValArgGlyPheIleThrGlyGlyTyrHis 368
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
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2.568
78.571
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3.562
72.727
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                                                                                                                                         Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 619
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6
                                                                                                                                                                                                                20-Aug-1999 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1588
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Gaps:
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0
36.364
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1
39.286
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5-exoprolinase (ATP-hydrolyzing) (EC 3.5.2.9) - rat
N;Alternate names: pyroglutamase (ATP-hydrolyzing)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-May-2000
C;Accession: T42756
R;Ye, G.J.; Breslow, E.; Meister, A.
J. Biol. Chem. 271, 32293-32300, 1996
A;Title: The amino acid sequence of rat kidney 5-oxo-L-prolinase determined by cDNA c
A;Reference number: Z22263; MUID: 97113037
A;Accession: T42756
                                               seq_documentation_block:
hypothetical protein Y47H9C.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-1288 <restyle="font-size: 1286;">LEGS A;Residues: 1-1288 <restyle="font-size: 1286;">LEBL:U70825; NID:g1732064; PID:g1732065; PIDN:AAC52955.1
A;Cross-references: EMBL:U70825; NID:g1732064; PID:g1732065; PIDN:AAC52955.1
A;Experimental source: strain Sprague-Dawley; Kidney
C;Superfamily: hypothetical protein YKL215c
C;Keywords: homodimer; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79584.1; PID:d1043370; PID:g
A;Experimental source: strain K1
C;Genetics:
C;Accession: T26971
R;Harris, B.
                                                                                                                                                                                       seq_name: pir2:T26971
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T42756 from: 1 to: 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                  215 HisValSerLeuSerSerGluValMetProMetValArgIleValProAr 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 rCysSerProArgIleAlaAlaLeuGly 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 TrpGluProIleAspAlaValPheLysValGluIleGluLeuAspArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
                                                                                                                                                                                                                                                                                              42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 GTGCAGCCCTCGCATTGCGCCATTAGGT 39
                                                                                                                                                                                                                                         gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
                                                                                                                                                                                                                                                                                                                                                                                                    CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCATT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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2.800
66.667
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3.111
69.231
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Gaps:
Percent Identity:
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0
38.462
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hypothetical protein F15E6.1 - Caenorhabditis elegans
(Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32633
R;Miller, N.; Stellyes, L.; Bradshaw, H.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F15E6.
A;Reference number: Z21202
A;Accession: T32633
                                                                                                                                                                                                                                                       alignment_block:
US-09-684-016-48411 x T32633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AF038614; PIDN:AAB92063.1; GSPDB:GN00022; CESP:F15E6.1 A;Experimental source: strain Bristol N2; clone F15E6 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 4
A; Introns: 16/1; 68/1; 190/3; 301/2; 602/3; 1203/3; 1295/1; 1554/3; 1642/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1655 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: Y47H9C.2
A; Map position: 1
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A; Cross-references: EMBL; AL032657; PIDN: CAA21738.1; GSPDB: GN00019; CESP: Y47H9C.
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A;Reference number: Z20293
A;Accession: 726971
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: CESP:F15E6.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:T32633
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                                                                                                                                                                                                      Align seg 1/1 to: T32633 from: 1
                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-684-016-48411/rev x T26971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: T26971 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
836 uGlyCysLysThrTrp 841
                                                                                                      821 CysHisCysGlyMetAspHisGlyAspGlyAspThrIle...GluCysGl 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 GluHisValLysMetLysTyrCysThrThrCysArgLeuTyrArgProPr 175
                                                   58 GGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 GCAGCCCTCGCATTGCGCCATT 43
                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oArgCysSerHisCysAlaIle 182
                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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3.438
66.667
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4.192
59.091
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Gaps: 0
Percent Identity: 45.833
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                                                                                                                                                                                                      to: 1655
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A;Molecule type: DNA
A;Residues: 1-46;47-64;65-101;102-118;119-132;133-147;148-161;162-173;174-185;186-19
A;Cross-references: GB:M89923
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Shelness, G.S.; Kanwar, Y.S.; Blobel, G.
J. Biol. Chem. 263, 17063-17070, 1988
A;Title: cDNA-derived primary structure of the glycoprotein component of canine A;Reference number: A31788; MUID:89034208
A;Accession: A31788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: An analysis of the complete sequence of a sugarcane bacilliform virus genome A;Reference number: PQ0542; MUID:93139779
A;Accession: PQ0542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyprotein - sugarcane bacilliform virus (fragments)
C;Species: sugarcane bacilliform virus
C;Species: sugarcane bacilliform virus
C;Datc: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
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A;Residues: 1-180 <SHE>
C;Keywords: glycoprotein; hydrolase; transmembrane protein
C;Keywords: glycoprotein; hydrolase; transmembrane protein
F;141/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
seq_documentation_block:
signal peptidase (EC 3.4.99.-) (SPC 22/23) - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 21-May_1990 #sequence_revision 21-May-1990 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Bouhida, M.; Lockhart, B.E.L.; Olszewski, N.E.
J. Gen. Virol. 74, 15-22, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: PQ0542
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                                                                                                                                                                                                                      Align seg 1/1 to: PQ0542 from: 1 to: 199
                                                                                                                                                                                                                                                                            US-09-684-016-48411 x PQ0542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-684-016-48411 x A31788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
63 sSerCys 65
                                                      58 GGGCTGC 64
                                                                                                            47 CysArgCysTyrValCysGlySerProAspHisLeuMetLysAspCysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 AspIleThrAlaAspLeuGluAsnIlePheAspTrpAsnValLysGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                             8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uPheLeuTyrLeuSerAlaGluTyrSerThrLys 96
                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
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Gaps: 0
Percent Identity: 42.857
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42.105
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seq_name: pir2:B86073

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seq_documentation_block:
    hypothetical protein mobA [imported] - Escherichia coli (strain 0157:H7)
    C:Specles: Escherichia coli
    C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001
    C:Accession: B86073
    R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL:L19201; NID:g304961; PIDN:AAB02992.1; PID:g304963
A:NOte: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: E65190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 06-Oct-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999 C;Accession: S40803; E65190  
R;Plunkett III, G; Burland, V; Daniels, D.L.; Blattner, F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-684-016-48411 x B86073
                                                                                    alignment_scores:
                                                                                                                                                                            A;Gene: mobA
A;Start codon: GTG
                                                                                                                                                                                                                                                           A; Experimental source: strain
                                                                                                                                                                                                                                                              A;Cross-references: GB:AE000461; GB:U00096; NID:g2367318; PIDN:AAC76855.1; PID:g1790288
A;Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-194 <BLAT>
                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; nucleic acid sequence not shown; translation not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 21, 3391-3398, 1993
A;Title: Analysis of the Escherichia coli genome. III. DNA sequence of the region A;Reference number: S40802; MUID:93347969
A;Accession: S40803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N; Alternate names: mob protein C; Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
molybdopterin-guanine dinucleotide biosynthesis protein A - Escherichia coli
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A;Molecule type: DNA
A;Residues: 1-194 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-194 <PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: nucleic acid sequence not shown; translation not shown
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   Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheCysProCysAspThrProTyrIleProHisAspLeuAlaAlaArg 112
                                                         Quality:
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                              Ratio:
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Percent Identity:
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   A;Cross-references:
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Nature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete,
A; Reference number: A70100; MUID:98065943
A; Accession: H70109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
ABC transporter, ATP-binding protein homolog - Lyme disease spirochete
C:Species: Borrella burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 02-Feb-2001
C:Accession: H70109
                                                                                           A; Reference number: Z22000
A; Accession: T41530
                                                                                                                                            C;Accession: T41530
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                        C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: ATP; nucleotide binding; P-loop
F;38-235/Domain: ATP-binding cassette homology <ABC>
F;55-62/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Nature 390, 580-586, 1997
A; Molecule type: DNA
A; Residues: 1-721 <W
                                                                                                                                                                                                                                                                                                      seq_documentation_block:
hypothetical protein SPCC645.13 - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                           seq_name: pir2:T41530
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A; Residues: 1-240 <KLE>
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US-09-684-016-48411 x S40803
                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 sGlyGluPheIleSerIleGlnGlyLysSerGlyCysGlyLysSerThrL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 CAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCTCACA 14
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PID:9268

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EMBL:AL049498; PIDN:CAB39909.1; GSPDB:GN00068;

SPDB: SPCC645.13

972h-; cosmid c645

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probable sucrose synthase (EC 2.4.1.13) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: sucrose synthase; 'sucrose/sucrose-phosphate synthase homology C;Keywords: glycosyltransferase; hexosyltransferase F;282-757/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:Buchner, P. submitted to the EMBL Data Library, October 1997 A; Reference number: Z15720 A; Accession: T06497
seq_name: pir2:T16487
                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-684-016-48411/rev x T06497
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    Quality:
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A; Residues: 1-809 <BUC>
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US-09-684-016-48411 x T41530
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                                                                                                                                                                                                                                                                                                                               105 GAAGATAAGTATCACCTTACATGTGAA......
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                                                                                                                           hrLysAsnThrIleGlyGlnTyrGluSerHisThrAlaPheThrLeuPro 506
                                                                                                                                                                                                       ||||||||::::::
tAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAlaGlyT 490
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                                                                                                                                                                                                                                                                                     GluAspLysTyrHisPheSerCysGlnPheThrAlaAspLeuIleAlaMe 473
                                                                                  GGGTTGTAAGGCATCTCACAT 13
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Gaps: 2
Percent Identity: 26.316
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36.364
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A;Cross-references: GB:M29004; NID:g161463; PID:g161464
A;Otoss-references: GB:M29004; NID:g161463; PID:g161464
A;Note: the publication does not report the complete sequence
C;Superfamily: unassigned EGF-related proteins; EGF homology
F;1-18/Domain: signal sequence *status predicted <SIG>
F;19-325/Product: exogastrula-inducing protein *status predicted <EGIP>
F;47-104/Product: EGIP petide C *status predicted <EGIC>
F;52-90/Domain: EGF homology <EG1>
F;106-156/Product: EGIP petide D *status predicted <EGID>
F;111-151/Domain: EGF homology <EG2>
F;117-228/Product: EGIP petide A *status predicted <EGIA>
F;182-223/Domain: EGF homology <EG3>
F;250-309/Product: EGIP petide B *status predicted <EGIB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exogastrula-inducing protein (EGIP) precursor - sea urchin (Strongylocentrotus purpun N;Alternate names: epidermal growth factor-sea protein N;Contains: EGIP peptide A; EGIP peptide B; EGIP peptide C; EGIP peptide D C;Species: Strongylocentrotus purpuratus (purple urchin) C;Date: 20-Mar-1992 #sequence_revision 15-Aug-1997 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Unusual pattern of accumulation of mRNA encoding A;Reference number: A40084; MUID:90049203 A;Accession: A40084
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A;Introns: 21/3; 45/2; 100/3; 147/3; 177/3; 232/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F56F10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 04-Mar-2000
C;Accession: T16487
                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-325 < YAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Yang, Q.; Angerer, L.M.; Angerer, R.C. Science 246, 806-808, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, March A; Description: The sequence of C. elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATCTCACATT 12
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cosmid F56F10
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sea

F;256-292/Domain: EGF homology <EG4>F;52-65,59-75,77-90,111-124,118-137,139-151,182-195,189-209,211-223,256-269,263-278,280

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C;Accession: D96660
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
                                                                                                                                                                                                                          seq_documentation_block:
protein F2K11.14 [imported] - Arabidopsis thaliana
protein F2K11.14 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T38168
R; Devlin, K.; Churcher, C.M.;
submitted to the EMBL Data Lih
A; Reference number: Z21775
A; Accession: T38168
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US-09-684-016-48411 x T38168
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seq_documentation_block:
hypothetical protein SPAC22E12.11c - fission yeast (Schizosaccharomyces pombe
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                            seq_name: pir2:D96660
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A; Residues: 1-859 <DEV>
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3.679
63.636
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Library, March 1996
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Conway, A.R.; C:
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                            Southwick,
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                                                                                                                                                                 l, S.; White, O.;
Creasy, T.H.; Dev
                               A.M.; Sun, H.; Tallon,
                                                                        Khaykin, E.; Kim, C
Maiti, R.; Marziali
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ewar, K.,
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A; Gene: :
A; Map po:
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A;Molecule type: DNA
A;Residues: 1-1518 <STO>
A;Cross-references: GB:A
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A;Accession: D96660
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A; Introns: 46/2; 84/3
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A; Residues: 1-95 <WIL>
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R; McMurray, A.
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US-09-684-016-48411 x D96660
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                                                                                                                                                                                                                                                           US-09-684-016-48411/rev x T26611
                                                                                                                                                                                                               Align seg 1/1 to: T26611 from: 1
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1411 HisCysIleCysLeuLysProTyrAsnSerArgSer...MetValSerCy 1426
                                                                                                                                                                    122 GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTAC
22 CATCTCAC 15
                                     56 ....GlnCysAspGlyAsnIleLeuProGlnLysHisGlnGlyPheTyrA 71
                                                                                72 CAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGG
                                                                                                                          46 IleLeuTrpAsnAsnIleLeuValMetIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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rgPheHis

73

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C;Species: Escherichia coli (;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001 C;Accession: B85615 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, 11ler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Description: terminal reductase during anaerobic growth on various sulfoxide an A, Note: chain A binds molybdopterin, chain B is an eletronen transfer protein, an C, Superfamily: nrfC protein; ferredoxin 2/4Fe-45] homology C; Keywords: 4Fe-45; heterotrimer; iron-sulfur protein; metalloprotein; oxidoreduce; 2-205/Product: dimethylsulfoxide reductase chain B #status experimental <MAT> F; 7-87/Domain: ferredoxin 2/4Fe-45] homology <FERL> F; 92-153/Domain: ferredoxin 2/4Fe-45] homology <FERC> F; 14, 17, 20, 79/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted F; 24, 67, 70, 75/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted F; 99, 102, 105, 145/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted F; 109, 126, 129, 141/Binding site: 4Fe-45 cluster (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            anaerobic dimethylsulfoxide reductase (EC 1.-.-.) chain B - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 11-Jun-1999 C;Accession: F64828; S03786; Q90169 C;Accession: F64828; S03786; Q90169 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, A.; Rose, D.J.; Mau, B.; Shao, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 20 min C;Complex: heterotrimer; chains A, B, and C;Function:
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A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: F64828
                                                                                                                                                                                                                                                                             seq_name: pir2:B85615
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A;Residues: 1-170, 'RA',171-205 <BIL>
A;Cross-references: GB:J03412; NID:gl
A;Note: part of this sequence, included
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Nucleotide sequence of the dmsABC operon encoding the anaerobic dimethylsulphova; Reference number: S03784; MUID:89096500 A;Accession: S03786
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                                                                                                                                                                       hypothetical protein dmsB [imported] -
                                                                                                                                                                                                              seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                            rLysGlyHisMetThrLysCysAspGlyCysTyrAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTA.....
                                                                                                                                                                                                                                                                                                                                                                                                              ....ATGGCGCAATGCGAGGGCTGCACTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Identity:
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                                                                                                                                                                       Escherichia coli (strain 0157:H7)
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   J.D.; Rose, Potamousis,
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   D.J.;
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   .; Mayhew Apodaca,
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   seq_name: pir2:T04224
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A;Cross-references: GB:AE005174; NID:g12514060; PIDN:AAG55382.1; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
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A;Introns: 61/1; 83/3
C;Superfamily: Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-245 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, June 1996 A; Reference number: 219454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F32D8.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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US-09-684-016-48411 x B85615
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A; Accession: T21654
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A; Residues: 1-205 <STO>
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                                          52 ATGCGAG...GGCTGCACT 67
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                                                                                       71 HisCysAlaCysGluSerThrCysAsnAsnProAspProTyrCysSerLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTA.....
                                                                                                                                5 TATTGTAAATGTGAGATGCCT...TACAACCCTGATGACCTAATGGCGCA 51
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sCysGluProGlyCysThr 93
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MUID:21074935; PMID:11206551
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34.483
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seq_documentation_block:
    adenylosuccinate lyase (EC 4.3.2.2) - chicken
    C:Species: Gallus gallus (chicken)
    C:Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 21-Jul-2000
    C:Accession: A35291
seq_name: pir2:F71844
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US-09-684-016-48411/rev x A35291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Aimi, J.; Badylak, J.; Williams, J.; Chen, Z.; Zalkin, H.; Dixon, J.E.
J. Biol. Chem. 265, 9011-9014, 1990
A;Title: Cloning of a cDNA encoding adenylosuccinate lyase by functional complementation A;Reference number: A35291; MUID:90264380
A;Accession: A35291
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US-09-684-016-48411 x T04224
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C; Superfamily: caffeoyl-CoA 3-O-methyltransferase
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A; Accession: T04224
A; Molecule type: DNA
A; Residues: 1-396 <BEV>
A; Cross-references: EMBL: AL049500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T5C23.200 - Arabidopsis thaliana c;SpecLes: Arabidopsis thaliana (mouse-ear cress) c;Date: 30-Apr-1999 #sequence_revisions 30-Apr-1999 #text_change 24-Nov-1999 C;Accession: T04224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-459 < AIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: pir2:A35291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone T5C23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; submitted to the Protein Sequence Database, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                          58
                                                 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 TGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGGC
                                                 sProLysAlaAlaAlaIleIleHisLeuGlyAlaThrSerCysTyrVal
                                                                                            CCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCTCACATT 12
                                                                                                                                           LysLeuArgHisAspValMetAlaHisValHisThrPheAlaHisCysCy 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CysAsnMetProTyrLeuProAspAspLeuLeuLeuAsnIleLeuGly 25
                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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                                                                                                                                                                                                                                            to: A35291 from: 1
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2.550
60.606
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4.250
75.000
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Gaps: 0
Percent Identity: 56.250
                                                                                                                                                                                                                                                                                                                                                                 Percent Identity:
                                                                                                                                                                                                                                            to: 459
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27.273
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                                                                     alignment_scores:
Ratio:
Percent Similarity:
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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein AAR21600.1 (imported) - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Accession: H86457
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio:
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A; Molecule type: DNA
A; Residues: 1-578 <ARN>
A; Cross-references: GB:AE001541; GB:AE001439; NID:g4155724; PIDN:AAD06712.1;
A; Cross-references: Strain J99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric p A;Reference number: A71800; MUID:99120557
A;Accession: F71844
                                                                                                   A; Molecule type: DNA
A; Residues: 1-697 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-684-016-48411/rev x F71844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABC transporter, ATP-binding protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 17-Mar-2000
                                                                   A;Cross-references: GB:AE005172; NID:g10645488; PIDN:AAG21600.1; GSPDB:GN00141
                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene:
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ABC transporter, ATP-bin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: F71844 from: 1 to:
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                                   Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      position:
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2.684
61.290
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0
38.710
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Quality:

51.00 3.643 50.000

Length: 28
Gaps: 1
Percent Identity: 35.714

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R:Newsome, A.L.; McLean, J.W.; Lively, M.O.

Blochem. J. 282, 447-452, 1992

A;Title: Molecular cloning of a cDNA encoding the glycoprotein of hen ovi
A;Reference number: S22412; MUID:92189580

A;Accession: S22412
A;Molecule type: mRNA
A;Residues: 1-180 <NEW1>
A;Cross-references: EMBL:X60795; NID:g63421; PIDN:CAA43208.1; PID:g63422
                                                                                                                                                                                                                               C:Species: Gallus gallus (chicken)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000
C:Accession: S22412; S40018; S15551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:C27H5.5
A;Introns: 27/2; 93/3; 203/1; 336/1; 358/2; 394/3; 473/2; 489/3; 531/3; 574/2; 636/3; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-1332 <PAU> A;Cross-references: EMBL:U14635; NID:g540265; PID:gA;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Pauley, A.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid C27H5.
A;Reference number: Z18386
A;Accession: T15670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C27H5.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15670
                                                                                                                                                                                                                                                                                                                seq_documentation_block:
signal peptidase (EC 3.4.99.-), microsomal - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-684-016-48411/rev x T15670
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US-09-684-016-48411 x H86457
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622 pGlyCysGlyValTrp.....HisHisThrArg 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:::|||
|yrThrThr 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gTyrPrometAspHisGlnAsnCysGluIleAlaPheAlaSerTyrAlaT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCACCTTACATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCG..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
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2.196
63.889
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6
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                                                                                                                                               of hen oviduct microsomal
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seq_documentation_block:
lipopolysaccharide heptosyltransferase (EC 2.4.99.-) II NMA1727 [similarity] -
c;Species: Neisseria meningitidis
c;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
c;Accession: B81869
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
lipopolysaccharide heptosyltransferase (EC 2.4.99.-) II rfaF [similarity] - |
C;Species: Neisseria gonorrhoeae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 21-Jul-2000
C;Accession: S61299
R;Schwan, E.T.; Robertson, B.D.; Brade, H.; van Putten, J.P.M.
Mol. Microbiol. 15, 267-275, 1995
Mol. Microbiol. 17aF mutants express Rd(2) chemotype LPS and do not enter
A;Reference number: S61299; MUID:95264913
A;Accession: S61299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:237141; NID:g599919; PIDN:CAA85504.1; PID:g599920 A;Note: the sequence of residues 1-2 are not shown in this paper C;Superfamily: ADP-heptose--LPS heptosyltransferase II C;Keywords: glycosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S40018
A;Molecule type: protein
A;Molecule type: protein
A;Mosidues: 1-15;36-45;50-58;76-83;97-118;141-160 <NEW2>
A;Residues: 91ycoprotein; hydrolase; transmembrane protein
E;1-180/Product: signal peptidase #status experimental <MAT>
F;141/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                   seq_name: pir2:B81869
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US-09-684-016-48411/rev x S61299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-336 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: S61299 from: 1 to: 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: S22412 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                            293 AspArgAlaLysIle...ValSerLeuHisLeuGlu...CysSerProCy 307
                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : ||||||||||::: ||||||||||::: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 AspIleThrAlaAspLeuGlnSerIlePheAspTrpAsnValLysGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                                                                                                                        sPheLysArgGluCysProLeuGlyHisThrAspCys 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pir2:S61299
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Swissprot_39:HIP1_HUMAN - 5
Swissprot_39:HRP1_SWISSPROT - 39:POEZ_CANFA + 5
Swissprot_39:MOBA_ECO57 + 5
Swissprot_39:MOBA_ECO57 + 5
Swissprot_39:MOBA_ECOLI + 5
Swissprot_39:EBP2_STRPU + 5
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Swissprot_39:EBP2_SWISSPROT_39:EBP1_MOUSE + 5
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SwissProt_39:MLO2_SCHPO
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Database sequences: 100059
Database length: 36664827
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Query: US-09-684-016-48411
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-Q-/c9n2_1/USPTC_spool/US99684016/runat_19032002_084440_20960/app_query.fasta_1.182
-Q-/c9n2_1/USPTC_spool/US99684016/runat_19032002_084440_20960/app_query.fasta_1.182
-DB=SwissProt_39 -QFMT=fastan -SUFFIX=std.rsp -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPEXT=4.000 -GAPEXT=0.000 -XGAPOP=10.000 -XGAPEXT=0.500
-FGAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALICN=200 -THR_SCORE=PCt
-THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE-LOCAL -OUTFHT=pfs
-NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09684016_@CGA1_1_28 -NOPU=6 -ICPU=3 -LONGLOG
-DELOF=100 -MAXLEN=200-THR_SCORE=-COCAL -USDANGENERAL -LONGLOG
-DELOF=100 -MAXLEN=2000000000
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n i Documentation
329 i Q09329 sch
192 i Q9jua5 nej
592 i Q31314 baj
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 | 000291 homo sapiens (human).
0 | P12280 canis familiaris (dog
1 | P58221 escherichia coli | 015/
4 | P58221 escherichia coli | 015/
4 | P32173 escherichia coli | 016/
5 | P15216 strongylocentrotus pu
1 | 010362 schizosaccharomyces f
2 | P1676 escherichia coli | and
3 | Q65944 canine adenovirus typ
4 | P18776 escherichia coli | and
5 | P21265 gallus gallus (chicke
2 | P06498 human adenovirus typ
6 | P28687 gallus gallus (chicke
2 | P08138 homo sapiens (human).
7 | Q921b8 mus musculus (mouse).
7 | Q43189 homo sapiens (human).
8 | Q9757 homo sapiens (human).
9 | Q9757 homo sapiens (human).
1 | Q43652 beta vulgaris (sugar
                                                                                                                                                                                                                                              0 1 Q03376 chironomus tentans (2 1 P29375 homo sapiens (human) 1 P21640 pseudomonas denitrifi 3 1 Q07092 homo sapiens (human) 1 P42948 saccharomyces cerevis Q173724 homo sapiens (human) 1 Q97210 mus musculus (mouse) 1 P20239 mus musculus (mouse) 1 P20239 mus musculus (mouse) 1 P32592 bost taurus (bovine) 1 P32592 bost taurus (bovine) 1 P32592 host sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 1 P32592 homo sapiens (human) 
                                                                                                                                                                           Q16635 homo sapiens (human).
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                Q25531 manduca sexta (tobacc
Q9nq69 homo sapiens (human).
Q9wuh2 mus musculus (mouse).
P18519 gallus qallus (chicke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q09329 schizosaccharomyces p
Q9jua5 neisseria meningitidi
O31314 bartonella bacillifou
Q91754 xenopus laevis (afric
            mus musculus (mouse) gallus gallus (chic)
                                                                                                                                                                                                            meleagris gallopavo
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            137 rMetPheGlnCysIleLeuCysGluAspTrp 147
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MLO2 OR SPBC4.05
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SwissProt_39:NGER_RAT +
SwissProt_39:AC3_HUMAN -
SwissProt_39:MM17_HUMAN -
SwissProt_39:APC2_CAVPO +
SwissProt_39:EGIP_ANTCR +
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                                                                                                                                                                                         US-09-684-016-48411 x MLO2_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00628; PHD; 1.
Pfam; PF02207; zf-UBRI; 1.
SMART; SM002249; PHD; 1.
SMART; SM00396; ZnF_UBRI; 1
SEQUENCE 329 AA; 38078 M
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                                              121 ArgPheCysIleCysAspThrValTyrAsnProGluThrGluGluGlyTh 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L42550; AAB41271.1; -. EMBL; AL121863; CAB58404.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McDougall R.C., Rajandream M.A., Barrell B.G., Brown S., Harris D.; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: NOT KNOWN, INTERFERE WITH MITOTIC CHROMOSOME SEGREGATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97128260; PubMed-8972853;
Javerzat J.-P., Cranston G., Allshire R.A.;
"Fission yeast genes which disrupt mitotic chromosome segregation when overexpressed.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetaes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seg
20-AUG-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003126; ZnF_UBR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001965; PHD.
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43 AATGGCGCAATGCGAGGGCTGCACTGACTGG 73
                                                                                      2 AGGTATTGTAAATGTGAGATGCCTTACAACCCT.....GATGACCT
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                                                                                                                                          to: MLO2_SCHPO from:
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1 099928 homo sapiens (hum
2 099129 homo sapiens (hum
2 090129 homo sapiens (hum
2 027916 cavia porcellus (
2 1 P15217 anthocidaris cras
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Seq_documentation_block:

ID MOBA_NEIMA STANDP
AC QDJUA5;
DT 20-AUG-2001 (Rel. 40,
DT 20-AUG-2001 (Rel. 40,
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DE MOBALE MOLYBDED;
RA ALGES K., MORTELLE RT "COMPLETE DNA SEQUENC
RA RAJANGARING MOLYBDED;
CC -1- SUNCTION: LINKS &
CC -1- FORMING MOLYBDED;
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At Alee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

An Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

An Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

An Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

An Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

An Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

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An Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

An Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Hall M.A.,

An Rajandream M.A., Simmonds M., Skelton J., Hall M.A.,

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Percent Similarity:
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                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CELL DIVISION PROTEIN FTSZ (75 KDA ANTIGEN).
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Bartonellaceae;
                                         Bacteria;
                                                                   Bartonella bacilliformis.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE MOLYBDOPTERIN-GUANINE DINUCLEOTIDE BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                            FTSZ_BARBA
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
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66.667
                         Rhizobiaceae group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                           .documentation_block:
    GCKR_XENLA STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell divi
NP_BIND
SEQUENCE
GCKR_XENLA STANDARD;
091754;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq)
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
-!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.

ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR, AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO BEGIN. BINDS TO AND HYDOLYZES GTP (BY SIMILARITY).

-!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: CYTOPLASMIC ASSEMBLE AT THE INNER SURFACE OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                        521 oGluAlaArgLeuGluProAlaValLysProLeuGlnAsnGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 GTGTGGAATAAATTGAAGATAAGTATCACCTTA.....CATGTGAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00423; CELLDVISFTSZ.
PROSITE; PS01134; FTSZ_1; 1.
PROSITE; PS01135; FTSZ_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000158; FtsZ.
InterPro; IPR003008; Tubul
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restricted the succession of the state of the succession of the state of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the succession of the su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97369823; PubMed=9226264; Padmalayam I., Anderson B., Kron M.,
                                                                                                                                                                                                                                                                                                                                               25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACCAGTCAGTGCAGCCCTCGCATTGCGCCCATTAGGTCATCAGGGTTGTA 26
                                                                                                                                                                                                                                                                                                                                               AGGCATCTCACATTTACAAT
                                                                                                                                                                                                                SwissProt_39:GCKR_XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              division;
                                                                                                                                                                                                                                                                                .GluSerHisIleTyrAsn
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2.173
65.000
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      Last sequence up
                                                                                                                                                                                                                                                                                   541
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   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-684-016-48411 x GCKR_XENLA
                                                                                                                                                                                            P97608;
15-DEC-1998
15-DEC-1998
15-DEC-1998
                                                                                                                                                                                                                                                                           documentation_block:
SEQUENCE FROM N.A., AND PARTIAL SEQUE
STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney;
MEDLINE-97111037; PubMed-8943290;
Ye G.-J., Breslow E., Meister A.;
                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                         OPLAH.
                                                                                                                                                                            5-OXOPROLINASE (EC
                                                                                                                                                                                                                                                            OPLA_RAT
                                                                                                                                                                                                                                                                                                                                               357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ProDom; PD025295; GCKR; 1.
PROSITE; PS01272; GCKR; 1.
SEQUENCE 619 AA; 68738 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch):
                                                                               NCBI_TaxID=10116;
                                                                                                                                                             (5-OPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X80901; CAA56863.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphate-insensitive regulatory protein of glucokinase.";
Eur. J. Biochem. 225:43-51(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Veiga-Da-Cunha M., Detheux M., Watelet N., van Schaftingen ^nCloning and expression of a Xenopus liver cDNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=95010134; PubMed=7925465;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR). Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE SIS FAMILY. GCKR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                              50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: INHIBITS GLUCOKINASE BY FORMING AN INACTIVE
                                                                                                                                                                                                                                                                                                                                                                            CAATGCGAGGGCTGCACTGACTGGTAAGTTTCAC 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity:
                                                                                                                                                                                                                                                                                                                                              gAspValArgGlyPheIleThrGlyGlyTyrHis 368
                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTATTGTAAAT...GTGAGATGCCTTACAACCCTGATGACCTAATGGCG
                                                                                                                                                                                                                                                                                                          SwissProt_39:OPLA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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                                                                                                                                                                      (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
(Rel. 37, Last annotation update)
ASE (EC 3.5.2.9) (5-0XO-L-PROLINASE) (PYROGLUTAMASE)
                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.50
2.568
78.571
                                                                                                Rodentia;
                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent
                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41B72C1981D1BA52 CRC64;
                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 28
Gaps: 1
Identity: 39.286
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fructose-
                                                                                                Rattus
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alignment_block: us-09-684-016-48411/rev \times OPLA_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: OPLA_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                     documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERRATUM.

Ye G.-J., Breslow E., Meister A.;

J. Biol. Chem. 272:4646-4646(1997).

-!- FUNCTION: CATALYZES THE CLEAVAGE OF 5-OXO-L-PROLINE TO FORM L-
GLUTAMATE COUPLED TO THE HYDROLYSIS OF ATP TO ADP AND INORGANIC
           candidate gene in a CAG expansion.";
                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                    Homo sapiens (Human).

Metazoa; Chordata;
                                                                                                                                                                                         HIP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U70825; AAC52955.1; -
InterPro; IPR002821; Hydantoinase_A.
InterPro; IPR003692; Hydantoinase_B.
Pfam; PF01968; Hydantoinase_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by cDNA cloning.";
J. Biol. Chem. 271:32293-32300(1996).
                                                           Huq A.H.M.M., Nichol Hayden M.R.;
                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Last annotation update)
HUNTINGTIN INTERACTING PROTEIN 1 (HIP-I) (FRAGMENT).
                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                       215 HisValSerLeuSerSerGluValMetProMetValArgIleValProAr 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01968; Hydantoinase_A; Pfam; PF02538; Hydantoinase_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>-</del>
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          000291;
                                                                                                                                                                                                                                                                                        HIP1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                       231 gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                           "Genomic organization of the human HIP1 gene and its candidate gene in a family diagnosed with Huntington
                                                                                                                                                                                                                                                                                                                                                                                                       42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 CATGTGAAACTTACCAGTCAGTGCAGCCCT......CGCATTGCGCCCATT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: WELL EXPRESSED IN TESTIS, K
SIMILARITY: BELONGS TO THE OXOPROLINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHATE.

CATALYTIC ACTIVITY: ATP + 5-OXO-L-PROLINE + 2 H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PHOSPHATE + L-GLUTAMATE.
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MEDLINE-20515263; PubMed-=11063258;

Chopra V.S., Metzler M., Rasper D.M., Engqvist-Goldstein A.E.Y.,

Singaraja R., Gan L., Fichter K.M., McCutcheon K., Drubin D.,

Nicholson D.W., Hayden M.R.;

"HIP12 is a non-proapoptotic member of a gene family including H

an interacting protein with huntingtin.";

Mamm. Genome 11:1006-1015(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wanker E.E., Rovira C., Scherzinger E., Hasenbank Tait D., Colicelli J., Lehrach H.;
"HIP-I: a huntingtin interacting protein isolated hybrid system.";
                                                                                                      EMBL;
                                                                                                                                                                                                                        EMBL;
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Kalchman M.A., Koide H.B., McCutcheon K., Graham R.K., Nichol K.
Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C.,
Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M.R.;
"HIP1, a human homologue of S. cerevisiae Sla2p, interacts with
membrane-associated huntingtin in the brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 82-995 FROM MEDLINE-97285121; PubMec
                                                                                                                                                                                                                                                              send
                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1 INTERACTION IS INVERSELY CORRELATED TO THE LENGHT OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CYTOSPLASMIC. MEMBRANE-ASSOCIATED PROTEIN. ALTERNATIVE PRODUCTS: 2 ISOFORMS; HIP1-1 AND HIP1-2; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SLA2 FAMILY.
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                MEDLINE=89034208; pubMed=3053702; Shelness G.S., Kanwar Y.S., Blobel G.; CDNA-derived primary structure of the glycoprotein canine microsomal signal peptidase complex."; J. Biol. Chem. 263:17063-17070(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                          _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CONFLICT
SEQUENCE
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
                                                                                                                                                                           MOBA OR MOB OR CHLB OR NARB Escherichia coli 0157:H7.
                                                                                                                                                                                                                    20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last ann)
MOLYBDOPTERIN-GUANINE DINUCLEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                  Escherichia
                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                        SEQUENCE FROM N.A
                                                                                                                                   NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                            MOBA_ECO57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Hydrolase; Microsome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A31788;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; J04067; AAA30894.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                     85
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SUBUNIT: COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS AS THEY ARE TRANSLOCATED INTO THE LUMEN OF THE ENDOPLASMIC RETICULUM.
SUBUNIT: COMPLEX OF FIVE DIFFERENT PROTEINS: SPC25, SPC21, SPC18, AND SPC12.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MICROSON PTM: OCCURS IN 2 DIFFERENTIALLY GLYCOSYLATED FORMS (22 MEMBRANE SPC25)
                                                                                                                                                                                                                                                                                                                                                                   uPheLeuTyrLeuSerAlaGluTyrSerThrLys 96
                                                                                                                                                                                                                                                                                                                                                                                                AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                          AspIleThrAlaAspLeuGluAsnIlePheAspTrpAsnValLysGlnLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER VERTEBRATES SPC22/23 AND TO YEAST SPC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       requires a
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144
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                                                                                                                                                                                                                                                                                              STANDARD;
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2.650
71.429
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164
141
141
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20313
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                                                                                                                                                                                                                Last sequence update)
Last annotation update)
DINUCLECTIDE BIOSYNTHESIS PROTEIN
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CYTOPLASMIC (POTENTIAL)
                                                                                                                                                              gamma
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N -> E (IN REF. 1; AA SEQUENCE).
342AB8E0F3F6D71A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                               subdivision; Enterobacteriaceae;
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Identity: 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 180
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                 MOBA_ECOLI STANDARE
P32173; Q9LBV0;
01-OCT-1993 (Rel. 27, C
01-OCT-1993 (Rel. 27, C
20-AUG-2001 (Rel. 40, I
MOLYBDOPTERIN-GUANINE E
                                                                                                                                                   _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
 Escherichia
              Bacteria;
                          Escherichia
                                       MOBA OR MOB OR CHLB
                                                                                                                                                                                                                                                                                                                                                                                                                         Molybdenum cofactor biosynthesis; GTP-binding; SEQUENCE 194 AA; 21629 MW; E6F2ABDEC7BA2205
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohnishi M., Murata T., Nakayama K., Kuhara S.,
Kurokawa K., Yasunaga T., Makino K., Shinagawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 87-194 FROM N.A. STRAIN=0157:H7 / RIMD 0509952;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                         97 PheCysProCysAspThrProTyrIleProHisAspLeuAlaAlaArg
                                                                                                                                                                                                                                     5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE MOBA FAMILY.
                                                                                                                                                                               SwissProt_39:MOBA_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE005616; AAG59046.1; -. AP002567; BAB38203.1; -. AB035920; BAA93557.1; -.
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             Proteobacteria;
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                                                                                                                                        STANDARD;
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11; PubMed=11258796;
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4.727
68.750
                                       OR NARB OR B3857.
                                                                   Last sequence update)
Last annotation update)
DINUCLEOTIDE BIOSYNTHESIS
                                                                                                             Created)
             gamma
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Percent Identity:
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             subdivision;
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              Enterobacteriaceae;
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H., Hayashi T.,
e determination
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MOBA_ECOLI

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194

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alignment_block:
US-09-684-016-48411
                                                                        alignment_scores:
                                                                                                                  Percent
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                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entities requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                     EMBL; L19201; AAB02992.1; -. EMBL; AE000461; AAC76855.1; -. PIR; S40803; S40803.
                                                                                                                                                                                                                                                                                                                                    This
                                                                                                                  SEQUENCE
                                                                                                                           Molybdenum cofactor biosynthesis; GTP-binding; Magnesium; 3D-structure; Complete proteome.
                                                                                                                                                      EcoGene;
                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lobbi-Nivol C., Palmer T., Whitty P.W., McNairn E., Boxer D.H.; "The mob locus of Escherichia coli K12 required for molybdenum cofactor biosynthesis is expressed at very low levels."; Microbiology 141:1663-1671(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmer T., Vasishta A., Whitty P.W., Boxer D.H.; "Isolation of protein FA, a product of the mob locus molybdenum cofactor biosynthesis in Escherichia coli. Eur. J. Biochem. 222:687-692(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-K12 / MG1655;
MEDLINE-93347969; PubMed-8346018;
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
Plunkett of the Escherichia coli genome. III. DNA sequence of the
"Analysis of the Escherichia coli."
"Analysis of the Scherichia".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lake M.W., Temple C.A., Rajagopalan K.V., Schindelin H.; "The crystal structure of the Escherichia coli MobA protein provides insight into molybdopterin guanthe dinucleotide biosynthesis."; J. Biol. Chem. 275:40211-40217(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
MEDLINE=20568278; PubMed=10978347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96004466; PubMed=7551035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-5, AND CHARACTERIZATION MEDLINE=94291668; PubMed=8020507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: LINKS A GUANÓSINE 5'-PHOSPHATE TO MOLYDOPTERIN (MPT) FORMING MOLYBDOPTERIN GUANINE DINUCLEOTIDE (MGD). COFACTOR: REQUIRES MAGNESIUM FOR ACTIVITY. PATHWAY: MOLYBDENUM COFACTOR BIOSYNTHESIS. SUBUNIT: MONOMER.
                                     Similarity:
                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: CYTOPLASMIC. SIMILARITY: BELONGS TO THE MOBA FAMILY.
                                                                                                                                                                 1E5K; 11-NOV-00.
1FR9; 10-JAN-01.
1FRW; 10-JAN-01.
                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                Quality:
Ratio:
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                                                                                                                                                     EG11829; mobA.
                                                                                                                  194
                                                                                                            Complete proteome. 4 AA; 21643 MW; F
x MOBA_ECOLI
                                  52.00
4.727
68.750
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                                     Percent
                                                                                                               B79B32DD7348DD48 CRC64;
                                     Identity:
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                                     50.
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alignment_block:
US-09-684-016-48411/rev x SUS2_PEA
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                                                                                                                                                                                                                    EMBL; AJ001071; CAA04512.1; InterPro; IPR001296; Glycos_transf_1.InterPro; IPR000368; Sucrose_synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
eurosids I; Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SUCROSE SYNTHASE 2 (EC 2.4.1.13) (SUCROSE-U
                                                                                             473 tAsnAsnAlaAspPheIleIleThrSerThrTyrGlnGluIleAlaGlyT
                                                                                                                                                                                        457 GluAspLysTyrHisPheSerCysGlnPheThrAlaAspLeuIleAlaMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Glycosyltransferase; Multigene fami
SEQUENCE 809 AA; 92208 MW; 6C5BBF708C37DE75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of a cDNA encoding synthase gene in pea (Pisum sativum L.).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. FRISSON;
Buchner P., Poret M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pisum sativum (Garden pea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (In) Plant Gene Register PGR98-105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.

CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE = 1
hrLysAsnThrIleGlyGlnTyrGluSerHisThrAlaPheThrLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO OTHER PLANTS SUCROSE SYNTHASE.
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                                                                                                                                                                                                                                                                                         1/1
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C 2.4.1.13) (SUCROSE-UDP
                                                . CAGCCCTCGCATTGCGCCATTAGGTCATCA
                                                                                                                                                                                                                                                                                           from:
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DE75 CRC64;
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_documentation_block:

507

GlyLeuTyrArgValValHis

513

SwissProt_39:FBP2_STRPU

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alignment_scores:
Quality:
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Percent Similarity:
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBP2_ST
P15216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-FEB-1996
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51.50
4.682
78.571
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33, Last annotation update)
ECURSOR (EPIDERMAL GROWTH FACTOR-RELATED
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91
152
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Percent Identity: 64.286
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                   Length:
Gaps:
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MBL outstation -
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seq_name: SwissProt_39:HEX9_ADECC
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US-09-684-016-48411 x FBP2_STRPU
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                                                                                                                                                                                                                                                                                      Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00249; PHD; 1.
SMART; SM00317; SET; 1.
PROSITE; PS50280; SET; 1.
Hypothetical protein; Zinc-finger.
Hypothetical Protein; 2inc-finger.
SEQUENCE 859 AA; 94886 MW; B486
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YDBB_SCHPO STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 94.9 KDA PROTEIN C22E12.11C IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q10362;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z70043; CAA93898.1; -. InterPro; IPR001965; PHD. InterPro; IPR001214; SET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi;
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                           21 uSerCysGluValTrp 26
                                                                                                           11 AAATGTGAGATGCCTTACAACCCTGATGAC...CTAATGGCGCAATGCGA
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                                                                                ArgCysValCysProPheGluAspAspAspGlyPheThrIleGlnCysGl
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3.679
63.636
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US-09-684-016-48411
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HEX9_ADECC STANDARD;
                                                                                                                                                          documentation_block:
                                       DMSB_ECOLI STANDARD; PRT; 204 AA P18776; P77745; 01-NOV-1990 (Rel. 16, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation updat ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIREDUCTASE IRON-SULFUR SUBUNIT).

DMSB OR B0895.
Escherichia coli.
Bacteria; Proteok
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97275900; PubMed-9129661;
MORTISON M.D., Onions D.E., Nicolson L.;
"Complete DNA sequence of canine adenovirus type 1.";
J. Gen. Virol. 78:873-878(1997).
-!- FUNCTION: THIS PROTEIN IS A STRUCTURAL COMPONENT OF THE VIRION.
MAY HAVE AN ADDITIONAL ROLE DURING ADENOVIRUS MULTIPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CLL;
Campbell J.B., Zhao Y.;
Submitted (AUG-1996) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canine adenovirus type 1 (strain CLL), Canine adenovirus type 1 (strain RI261) Viruses; dsDNA viruses, no RNA stage; ACBL_TaxID-69150, 69151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
HEXON-ASSOCIATED PROTEIN (PROTEIN IX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hexon-associated
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Ratio:
c Similarity:
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                                                                                                                                                                                                                    yAlaArgGlnAsnValThrGly
               Proteobacteria;
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Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=89096500; PubMed=3062312;
Bilous P.T., Cole S.T., Anderson W.F., Weiner J.H.;
Bilous P.T., Cole s.T., Anderson W.F., Weiner J.H.;
"Nucleotide sequence of the dmsABC operon encoding the anaerobic dimethylsulphoxide reductase of Escherichia coli.";
Mol. Microbiol. 2:785-795(1988).
                            InterPro; IPR001450; 4FE4S_ferrdxin.
Pfam; PF00037; fer4; 1.
                                                                                     EMBL; J03412; AAA83844.1; -.
EMBL; AE000191; AAC73981.1; -.
EMBL; D90727; BAA35627.1; -.
EMBL; S03786; S03786.
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A 718-kb DNA sequence of the corresponding to the 12.7-28.0 DNA Res. 3:137-155(1996).
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
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            PROSITE;
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EcoGene; EG10233; dmsB
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SIMILARITY: THE IRON-SULFUR CENTERS
'BACTERIAL-TYPE' 4FE-4S FERREDOXINS
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SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS:
REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN,
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                                                        COMPLEMENTATION IN ESCHERICHIA COLL.";

J. BIOL. Chem. 265:9011-9014(1990).

-!- CATALYTIC ACTIVITY: 1-(5-PHOSPHORIBOSYL)-4-(N-SUCCINO-CARBOXAMIDE)

-5-AMINOIMIDAZOLE = FUMARATE + 5'-PHOSPHORIBOSYL-5-AMINO-4-

IMIDAZOLECARBOXAMIDE (ALSO CATALYZES: N6-(1,2-DICARBOXYETHYL)AMP =
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01-MAY-1991 (Rel. 18, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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PRINTS; PR00149; FUMRATELYASE.

PROSITE; PS00163; FUMRATE_LYASES; 1

Purine biosynthesis; Lyase.

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SEQUENCE 459 AA; 51786 MW; E5EC1.
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E315_ADE05 STANDARD;
MEDLINE-92148953; PubMed-1531370; Krajcsi P., Tollefson A.E., Anderson C.W., Wold W.S.M.; Tollefson A.E., Anderson C.W., Which is required for "The adenovirus E3 14.5-kilodalton protein, which is required for down-regulation of the epidermal growth factor receptor and prevention of tumor necrosis factor cytolysis, is an integral membrane protein oriented with its C terminus in the cytoplasm."; J. Virol. 66:1665-1673(1992).
                                                                                                                                                             IDENTIFICATION OF PROTEIN.
MEDLINE-90177214; PubMed-2309441;
Tollefson A.E., Krajcsi P., Pursk
"A 14,500 MW protein in constant
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                                                                                                                                                                                                                                                                                                                      Human adenovirus type 5. Viruses; dsDNA viruses, no
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01-JAN-1988 (Rel. 06, Last
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                                                                                                           SIGNAL SEQUENCE CLEAVAGE SITE
                                                                                                                                                "A 14,500 MW protein adenoviruses.";
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                                                                                                                                                                          W.S.M.; -
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seq_documentation_block:
ID SPC2_CHICK STAN
AC P28687;
DT 01-DEC-1992 (Rel. 2
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SPC2_CHICK ST/
P28687;
01-DEC-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92263760; pubMed-1533979;
Krajcsi P., Tollefson A.E., Wold W.S.M.;
"The E3-14.5K integral membrane protein of adenovirus that is required for down-regulation of the EGF receptor and for prevention of TNF cytolysis is O-glycosylated but not N-glycosylated.";
Virology 188:570-579(1992).
                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chroboczek J., Bieber F., Jacrot B.;
"The sequence of the genome of adenovirus type 5 and its
with the genome of adenovirus type 2.";
Virology 186:280-285(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92087470; PubMed=1727603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 187:492-498(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krajcsi P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92188523;
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                                                                                                        34
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                                                                                                                                                                                                 66
                                                                                                                                      16
                                                                                                                                                                                                                             MetLysPheThrValThrPheLeuLeuIleIleCysThrLeuSerAlaPh
                                                                                                                                                                                                                                                      TTGAAGATAAGTATCACC.....TTACATGTGAAACTTACCAGTCA
                                                                                                                         ACATTTACAAT 6
                                                                                                                                                                    eCysSerProThrSerLysProGlnArgHisIleSerCysArgPheThrA
                                                                                                                                                                                                GTGCAGCCCTCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-GLYCOSYLATED.
SIMILARITY: TO EQUIVALENT PROTEIN IN OTHER ADENOVIRUSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e adenovirus E3-14.5K protein which is required for prevention of cytolysis and for down-regulation of the EGF receptor contains sphoserine ":
                                                                                                        rgIleTrpAsn 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: DOWN-REGULATES THE EGF RECEPTOR AND
                                                                          SwissProt_39:SPC2_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M73260; -; NOT_ANNOTATED_CDS X03002; CAA26786.1; -.
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Ratio:
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19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein; Phosphorylation;
                                STANDARD;
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2.196
62.162
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                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                 Identity:
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Gaps:
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seq_documentation_block:
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DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Newsome A.L., MCLUCAL CONA encoding the glycoprotein of nen Molecular cloning of a CDNA encoding the glycoprotein of nen microsomal signal peptidase.";
Blochem. J. 282:447-452(1992).
Blochem. J. 282:447-452(1992).
-1- FUNCTION: MICROSOMAL SIGNAL PEPTIDASE IS A MEMBRANE-BOUND ENDOPROTEINASE THAT REMOVES SIGNAL PEPTIDES FROM NASCENT ENDOPENDED INTO THE LUMEN OF THE
P08138;
01-AUG-1988 (Rel.
                             NGFR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- SUBUNIT: HEN OVIDUCT SIGNAL PEPTIDASE ACTIVITY IS ASSOCIATED WITH AN APPARENT COMPLEX OF OLLY TWO PROTEINS, WITH ESTIMATED MOLECULAR MASSES OF 19 AND 23 KDA.

-i- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MICROSOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-1992 (Rel. 15-JUL-1998 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICROSOMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lransmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GP23).
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                                                                                                                                                                                               38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                                 AspTleThrAlaAspLeuGlnSerIlePheAspTrpAsnValLysGlnLe
                                                                                                      uPheLeuTyrLeuSerAlaGluTyrSerThrLys
                                                                                                                                    AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MICROSOMAL. SIMILARITY: TO OTHER VERTEBRATES SPC22/23 AND TO YEAST SPC3
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                                                                         SwissProt_39:NGFR_HUMAN
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S22412; S22412.
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36, Last annotation update)
PEPTIDASE 23 KDA SUBUNIT (EC
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 Created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microsome; Endoplasmic reticulum; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
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; A5572439EB8210AA CRC64;
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; Galliformes; Phasianidae; Phasiani
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01-AUG-1988 (Rel. 08
20-AUG-2001 (Rel. 40
LOW-AFFINITY NERVE
(GP80-LNGFR) (P75 IC
NGFR OR TNFRSF16.
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                                                                                                                                                                                                                           PROSITE; PS00652; THER NGER 1; 3.

PROSITE; PS50050; THER NGER 2; 4.

PROSITE; PS50017; DEATH_DOMAIN; 1.

Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
                                                                                                                                                                                                                                                                            Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                   DOMAIN
                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                  Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                                                InterPro; IPR000488;
InterPro; IPR001368;
                                                                                                                                                                                                                                                                                                                                                                   PIR; A25218; GQHUN.
HSSP; P07174; 1NGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor gene.";
Mol. Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=89096903; pubMed=2850481;
Sehgal A., Patil N., Chao M.;
"A constitutive promoter directs expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression and structure of the human NGF receptor."; Cell 47:545-554(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-87051725; PubMed-3022937;
MEDLINE-87051725; PubMed-3022937;
                                                                                                                                                                                                                                                                                                                                                         MIM; 162010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson D., Lanahan A
Bothwell M., Chao M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOND FORMATION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.

SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND NT-3, AND NT-4.
SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol.
   29
251
273
31
31
108
148
344
344
47
67
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40, Last annotation update)
E GROWTH FACTOR RECEPTOR PRECURSOR
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Institute. There are no restrictions
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POTENTIAL.
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Quality:
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US-09-684-016-48411 x NGFR_HUMAN
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-NIH SWISS;
STRAIN-NIH SWISS;
Howard T.L., Ingermann A.R., Hollenberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                    MEDLINE-99018220; PubMed-9799836;
Kawakami S., Mitsunaga K., Kikuti Y.Y., Ando A., Inoko H.,
Yamamura K., Abe K.;
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHD FINGER PROTEIN 1 (PHF1 PROTEIN) (T-COMPLEX TESTIS-EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: TESTIS-SPECIFIC.
-!- SIMILARITY: CONTAINS 2 PHD-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Testis
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POLYCOMBLIKE 1) (MPCL1).
PHF1 OR TCTEX3 OR TCTEX-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9Z1B8; O54808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 GGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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427
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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interacts with polycomb-group
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; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001965; PHD.
InterPro; IPR00299; Tudor.
Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR; 1.
Nuclear protein; Zinc-finger; R
ZN_FING 89 142
PH
ZN_FING 188 237
CONFLICT 249 249
CONFLICT 344 344
CONFLICT 377 377
CONFLICT 555 555
CONFLICT 558 559
IF
                                                                                                                                                                                                                                                                                                                                                                           documentation_block:
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHD FINGER PROTEIN 1 (PHF1 PROTEIN).
                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2).
Wang J.H., Du G.W., Zhou Y., Yuan J.G., Qiang
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                 TISSUE=Placenta;
MEDLINE=98207256; PubMed=9545646;
                                                                                                                                                                                                                                                                                                                                                      PHF1_HUMAN
043189; 060929;
                                                                                                                                                       Genomics
                                                                                                                                                                   similarity
                                                                                                                                                                                        Coulson
                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                         204 sArgSerCysLeuGlnTrp 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrCysTyrCysGlyGlyProGlyGluTrpAsnLeuLysMetLeuGlnCy
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CGAGGGCTGCACTGACTGG
                                                                                                                                                              son M., Robert S., Eyre H.J., Saint in identification and localization of a larity to Polycombike of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                 SwissProt_39:PHF1_HUMAN
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; AB011550; BAA25074.1; -.
MGI:98647; Tctex3.
                                                                                                                                                      48:381-383(1998).
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PHD-TYPE 1.
PHD-TYPE 2.
L -> F (IN REF. 1).
G -> E (IN REF. 2).
R -> S (IN REF. 2).
G -> R (IN REF. 2).
G -> HLPDSLLLLPSPFTHWHFHAI
2).
M; 6D2EE5F53D6164C2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                   Saint R.;
ion of a human gene with sequence sophila melanogaster.";
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Identity:
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E (IN REF. 2).
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0
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                                                                                                       B.Q.;
databases.
                                     2/PHF2 (SHOWN HERE);
              SKELETAL MUSCLE,
    LIVER,
    AND
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seq_name:
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SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR; 1.
SMART; SW00333; TUDOR; 1.
Nuclear protein; Zinc-finger; R
Nuclear protein; Zinc-finger; R
ZN_FING 89 142
ZN_FING 188 237 PH
VARSPLIC 350 457 SF
                      Scanlan M.J.,
Jongeneel V.,
Old L.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            documentation_block:
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SEQUENCE
                                                                                                                                                                                                                                                                                            BS4_HUMAN STANDARD; PRT; 601 AA (9Y5A7; 095422; 20-AUG-2001 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation update) 20-AUG-2001 (Rel. 40, Last annotation
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EMBL;
                                                                                           SEQUENCE FROM N.A. MEDLINE-99438124; Pubmed-10508479;
                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                          NYREN18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204 sArgSerCysLeuGlnTrp 210
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567 i
                                             Gordan J.D., Williamson Gure A.O., Jager D., Jag
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3.571
60.870
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62077
                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
þγ
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SEPSGOGPGGGVSRPIGKRRRPEPEPLRRRQKGKVEELGPP
SAVRNQPEPQEQRERAHLQRALQASVSPPSPSPNQSYQGSS
GYNERPTDARCLPSSPIRMFASFHPS -> RAGPWGRGLTS
PGEAPEAGARAPEEEAEGESGGAGATLSSAQSARAPGAEGA
GSSAEGTAAAPSGCLLPSTLLPAPQGPLGTVDPQTGHPWNF
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MISSING (IN ISOFORM 1).
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Gaps:
t Identity:
                                                Jager E.,
  antibody
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E., Knuth
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patients
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                                                  Bander N.H.,
Chen Y.-T.,
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RRP RC
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15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
SUCROSE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                    _documentation_block:
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SEQUENCE
                                                                                               Beta vulgaris (Sugar beet).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                 SUSY_BETVU
Q42652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401
  TISSUE=Tap root;
                            SEQUENCE FROM N.A.
                                                                              NCBI_TaxID=3555;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368
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Pfam; PF00627; UBA; 2.
SMART; SM00165; UBA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 3 UBA DOMAINS.
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                                                                                                                                                                                                                                               (FRAGMENT).
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J. Cancer 83:456-464(1999).
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601
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(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
THASE (EC 2.4.1.13) (SUCROSE-UDP G
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UBA 2.
UBA 3.
D -> DNYRTTGIATIEVFLPPRLKKDLAKQYSDRLECCEN
EVEKVIEEIRCKAIERGTGND (IN REF. 2).
R -> K (IN REF. 2).
p5a6eCae0B3a975B CRC64;
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seq_name: SwissProt_39:BAR3_CHITE
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                                                                                                                                                     BAR3_CHITE STANDARI
Q03376;
01-OCT-1993 (Rel. 27, C
01-OCT-1993 (Rel. 27, I
01-OCT-1994 (Rel. 30, I
BALBIANI RING PROTEIN 3
                                                                                                                                                                                                                                                           documentation_block:
                                                                  Chironomus tentans (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Euterygota; Neoptera; Endopterygota; Diptera; Nematoce
Chironomoidea; Chironomidae; Chironominae; Chironomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Mol. Biol. 30:863-872(1996).

-i- FUNCTION: SUCROSE-CLEAVING ENZYME THAT PROVIDES UDP-GLUCOSE A FRUCTOSE FOR VARIOUS METABOLIC PATHWAYS.

-i- CATALYTIC ACTIVITY: UDP-GLUCOSE + D-FRUCTOSE = UDP + SUCROSE.

-i- TISSUE SPECIFICITY: EXPRESSED MOST PREDOMINANTLY IN TAP ROOT.
                                                                                                                                                                                                                                                                                                                               449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 415
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InterPro: IPR000368; Sucrose_synth.
Pfam; PP00534; Glycos_transf_1; 1.
Pfam; PP00862; Sucrose_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
TISSUE=Salivary gland;
                 SEQUENCE FROM N.A
                                                   NCBI_TaxID=7153;
                                                                                                                                                                                                                                                                                                                                                                                               432 hrLysAsnThrValGlyGlnTyrGluSerHisLysAlaPheThrPhePro 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
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vulgaris L.).";
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                                                                                                                                                                                                                                                                                                                                                                                                                                 63
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P2375;
01-DEC-1992 (Rel. 24, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-7001 (Rel. 40, PROTEIN 2 (RBBP-2).
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"The Balblani ring 3 gene in Chironomus tentans has a diverged repetitive structure split by many introns.";

J. Mol. Blol. 211:331-349(1990).

-i. FUNCTION: USED BY THE LARVAE TO CONSTRUCT A SUPRAMOLECULAR STRUCTURE, THE LARVAL TUBE. BALBIANI RING PROTEIN 3 COULD PLAY A ROLE AS A TRANSPORT PROTEIN THAT BINDS TO OTHER PROTEINS ROLE AS A TRANSPORT HOSCHUBLE FIBERS TO OTHER PROTEINS INTRACELULARLY AND IN THE GLAND LUMEN IN ORDER TO PREVENT THESE FROM FORMING WATER-INSOLUBLE FIBERS TOO EARLY.

-i. SUBCELULAR LOCATION: SECRETED.

-i. SUBCELULAR LOCATION: SECRETED.

-i. TISSUE SPECIFICITY: SALIVARY GLAND.
                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                            SEQUENCE FROM N.A.

MEDLINE-94020841; PubMed-8414517;

Fattaey A.R., Helln K., Dembski M.S., Dyson N.,

Vuocolo G.A., Hanobik M.G., Haskell K.M., Oliff

Jones R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro
"Characterization RBP2.";
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SIGNAL 1
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Paulsson G., Lendahl U., Galli J.,
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                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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             proteins RBP1
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COBJ_PSEDE STANDARD;
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                                                                                           01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
PRECORRIN-3B C17-METHYLIRANSFERASE (EC 2.1.1.131) (PRECORRIN-3
                                                      СОВЛ
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                          Pseudomonas
                                                                        METHYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S66431; AAB28544.1;
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                                                                                                                                                                                                                                                                                                                                                                            52 ATGCGAGGGCTGCACTGACTGG
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FACR 1566 MISSING (IN REF. 2).
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Bacteria;

Proteobacteria;

gamma subdivision; Pseudomonadaceae;

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seq_documentation_block:
ID CAIF_HUMAN STANDA
AC 007092;
DT 01-FEB-1995 (Rel. 31,
DT 01-FEB-1995 (Rel. 31)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Crouzet J., Cameron B., Cauchois L., Rigault S., Rouyez M.-C. Blanche F., Thibaut D., Debussche L.; "Genetic and sequence analysis of 8.7-kilobase Pseudomonas denitrificans fragment carrying eight genes involved in transformation of precorrin-2 to cobyrinic acid."; J. Bacteriol. 172:5980-5990(1990).
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                                                                                                                                                                                                                                                                                  103
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Cobalamin biosynthesis; Porphyrin biosynthesis; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; E36145; E36145.
InterPro; IPR000878; Corrin_porph_mthyltrnf.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=43306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriol. 175:7430-7440(1993).
- FUNCTION: METHYLTRANSFERASE THAT CATALYZES THE METHYLATION C-17 IN PRECORRIN-3B TO FORM PRECORRIN-4.
                                                                                                                                                                                                             aValAlaAlaArgIleGlyAlaProLeuGlyHisAspPheCysAlaIleS
                                                                                                                                            er
                                                                                                                                                                          CT
                                                                                                                                                                                                                                                                                                                   TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO S.TYPHIMURIUM CBIH; ALSO, LOW, METHYLASES INVOLVED IN COBALAMIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADENOSYL-L-HOMOCYSTEINE + PRECORRIN 4. PATHWAY: COBALAMIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE +
                                                                                                                                                                                                                                              GTGCAGCCCTCGCATT...GCGCCATTAGGTCATCAGGGTTGTAAGGCAT
                                                                                                                                                                                                                                                                                TrpLysSerValGluLeuValIleThrProGlyValThrAlaMetLeuAl 119
                                                                                                     SwissProt_39:CA1F_HUMAN
                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
(Rel. 31, Created)
(Rel. 31, Last sequence update)
                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                         49.50
2.475
58.824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27105 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 34
Gaps: 1
Percent Identity: 38.235
                                                                                                                                                                                                                                                                                                                                                       from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A30B027F4AFBE23F CRC64;
                                                                                                                                                                                                                                                                                                                                                    Н
                                                                                                                                                                                                                                                                                                                                                    to:
                                                      1603
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e of coenzyme
                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Blanche
ne B12 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRECORRIN-3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TO OTHER
                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                     67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
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DOMAIN
                                                                                                                                                                                                                                                                                                                              PIR; S23810; S23810.
MIM; 120326; -.
                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain, alpha 1(XVI), consisting of repetitive collagenous
cysteine-containing non-collagenous segments.";
J. Biochem. 112:856-863(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIINE=92335339; PubMed=1631157; Pan T.C., Zhang R.Z., Mattei M.-G., Timpl R., Chu M.-L.; "Cloning and chromosomal location of human alpha l(XVI) collagen."; Proc. Natl. Acad. Sci. U.S.A. 89:6565-6569(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, COLLAGEN ALPHA 1(XVI)
                                                                                                               DOMAIN
                                                                                                                                                                                                                                             SMART; SM00210;
                                                                                                                                                                                                                                                                Pfam;
                                                                                                                                                                                                                                                                              Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanamori T., Yamakoshi H., Nagai Y.;
"Molecular cloning and partial characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamaguchi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93203161; PubMed=1284248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COL16A1.
                                               DOMAIN
                                                             DOMAIN
                                                                                               DOMAIN
                                                                                                                                             DOMAIN
                                                                                                                                                                                                             Repeat;
                                                                                                                                                                                                                                Extracellular matrix; Connective tissue;
                                                                                                                                                                                                                                                                                             InterPro; IPR000087; Coll:
InterPro; IPR003129; TSPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 418-1603 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH OTHER TYPES OF COLLAGEN.

DEVELOPMENTAL STAGE: TRANSIENTLY ELEVATED EXPRESSION DURING

GESTATION, AND DECREASE AT TERM.

DOMAIN: THIS SEQUENCE DEFINES EIGHTEEN DIFFERENT DOMAINS, NINE

TRIPLE-HELICAL DOMAINS (COL9 TO COL1) AND TEN NONTRIPLE-HELICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMNION, IT IS FOUND IN AN ACELLULAR, RELATIVELY DENSE LAYER OF A COMPLEX NETWORK OF RETICULAR FIBERS. ALSO LOCATED TO A FIBROBLAST LAYER BENEATH THIS DENSE LAYER. EXISTS IN TISSUES IN ASSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE NUMEROUS INTERRUPTIONS IN THE TRIPLE HELIX MAY MAKE THIS MOLECULE EITHER ELASTIC OR FLEXIBLE.
TISSUE SPECIFICITY: IN THE PLACENTA, WHERE IT IS FOUND IN THE AMNION, A MEMBRANOUS TISSUE LINING THE AMNIOTIC CAVITY. WITHIN THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
SIMILARITY: BELONGS TO THE FAMILY OF FIBRIL-ASSOCIATED COLLAGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAINS (NC10 TO NC1).
PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTIW
                                                                                                                                                                                                                                                             PF01391; Collagen; 16. PF02210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                           M92642; AAA58427.1;
S57132; AAB25797.1;
                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERRUPTED HELICES (FACIT)
                                              555
572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Kimura S., McBride O.W., Hori H.,
Yamakoshi H., Nagai Y.;
                                                                                                                                                                                                                                               TSPN;
                                                                                                                                            21
1603
374
505
                                                                                                                                                                                                                                                                                                             Collagen
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                                                                                                                                                                                                                                                                                                                                                              .' .'
                              WITH 1
                                              TRIPLE-HELICAL REGION 7
                                                                              WITH 1
                                                                                              TRIPLE-HELICAL REGION 8 (COL8)
                                                                                                               NONHELICAL REGION 9
                                                                                                                            TRIPLE-HELICAL REGION 9 (COL9) WITH 3 IMPERFECTIONS.
                                                                                                                                                             COLLAGEN ALPHA 1(XVI) CHAIN. NONHELICAL REGION 10 (NC10).
TRIPLE-HELICAL REGION 6 (COL6)
               NONHELICAL REGION
                                                               NONHELICAL REGION
                                                                              IMPERFECTION.
                                IMPERFECTION.
                                                                                                                                                                                                                            Collagen; Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEN NONTRIPLE-HELICAL
                                                               8 (NC8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of a novel collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada Y.
                                                                                                               (NC9)
                                               (COL7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domains
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RET TREE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
      Rasmussen S.W.;
Rasmussen S.W.;
"A 37.5 kb region of yeast chromosome and CSD3 genes, a TCP-1-related gene, and CSD3 genes, and a tRNA(Arg).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 63.9 KDA PROTEIN IN IMEZ-MEF2 IN
                                                                                                                                                                                                                                                                                                                                                                                                       documentation_block:
  to the
Yeast 1
                                                                                             SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE-96090136; Pubh
                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                   Saccharomycetales;
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DOMAIN
                                                                                                                                                                                 NCBI_TaxID=4932;
                                                                                                                                                                                                                                                              YJL105W OR J0819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt rgProValGlyHisValPheLeuGlyLeuAspAlaGluGlnGlyLysPro}
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                                                                                                                                                                                                                                                                                                                                                                                    YEAST
  e DAL80 gene, and a
11:873-883(1995).
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Ratio:
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887
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                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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1.768
45.902
                                                                                                 PubMed=7483851;
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WITH 2 IMPERFECTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRIPLE-HELICAL REGION 5 (NC5).
WITH 2 IMPERFECTIONS.
NONHELICAL BETTONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH 2 IMPERFECTIONS.

NONHELICAL REGION 1 (NC1).

RDA -> GGR (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NONHELICAL REGION 4 (I
TRIPLE-HELICAL REGION
NONHELICAL REGION 3 (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRIPLE-HELICAL REGION 1 (COL1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WITH 3 IMPERFECTIONS NONHELICAL REGION 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRIPLE-HELICAL REGION 5 (COL5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NONHELICAL REGION 2 (NC2)
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NONHELICAL REGION 6 (NC6)
                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identity:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                    560
                                     an open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                                                        X includes the SME1,
                                                                                                                                                                                                     Saccharomyces
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                                                                                                                                                                                                                                                                                  INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
5
31.148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                        MEF2,
                                       similar
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seq_documentation_block:
ID GCS1_HUMAN STANDARD;
AC Q13724;
DT Q1.NOV-1997 (Rel. 35, Crea
DT 15-JUL-1998 (Rel. 40, Last
DT 20.AUG-2001 (Rel. 40, Last
DE MANNOSYI-OLIGOSACCHARIDE G
GLUCOSIDASE I).
GS GCS1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chorda
OC Mammalia; Eutheria; Primat
OX (Rel.TaxID-9806;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Hippocampus;
RX Alz-Fueller B., Bieberich
RT "Cloning and expression of
Eur. J. Biochem. 231:344-3
RN ERRATUM.
RA Kalz-Fueller B., Bieberich
RL Eur. J. Biochem. 231:344-3
RN ERRATUM.
RA Kalz-Fueller B., Bieberich
RL Eur. J. Biochem. 249:912-9
CC -i-FUNCTION: CLEAVES THE
CC SPECIFICALLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                             013724;
01-NOV-1997 (Rel. 35, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MANNOSYL-OLIGOSACCHARIDE GLUCOSIDASE (EC 3.2.1.106) (PROCESSING
                   Kalz-Fueller B., Bieberich E., Bause E.;
Eur. J. Biochem. 249:912-912(1997).
-!- FUNCTION: CLEAVES THE DISTAL ALPHA 1,2-LINKED GLUCOSE RESIDUE FROM THE GLC(3)MAN(9)GLCNAC(2) OLIGOSACCHARIDE PRECURSOR HIGHLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179
                                                                                                                                     Kalz-Fueller B., Bieberich E., Bause E "Cloning and expression of glucosidase Eur. J. Biochem. 231:344-351(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 CysIleCysGlySerSerAspSerLysAspGluLeuPheIleGlnCysAs 179
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical SEQUENCE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00249; PHD; 1
SMART; SM00317; SET; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGD; S0003641; YJL105W.
InterPro; IPR001965; PH
InterPro; IPR001214; SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: TO YEAST YKR029C AND S.POMBE SPAC22E12.11C
-i- SIMILARITY: CONTAINS 1 PHD-TYPE ZINC FINGER.
-i- SIMILARITY: CONTAINS 1 SET DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50280; SET;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SwissProt_39:GCS1_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: YJK5_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 protein; Zinc-finger
560 AA; 63855 MW; 9A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAA89400.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49.00
4.083
54.545
                                                                                                                                                                                                 PubMed=7635146;
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                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9A7BAECE97318AFA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identity:
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Gaps:
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0
36.364
                                                                                                                                                            human
                                                                                                                                                        hippocampus.";
                                                                                                                                                                                                                                                                                           Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                       7
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alignment_block:
US-09-684-016-48411/rev
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                                                                                                                                                                                                                                                                         _documentation_block:
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Rehli M., Den Elzen N., Cassady A.I., Ostrowski M.C., Hume D.A.; "Cloning and characterization of the murine genes for bHLH-ZIP transcription factors TFEC and TFEB reveal a common gene organization all MiT subfamily members.";
                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                   20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                          TFEB OR TCFEB.
                                                                                                                                                                                         TRANSCRIPTION FACTOR EB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endoplasmic reticulum.
DOMAIN 1 38
TRANSMEM 39 59
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                                                                          STRAIN=BALB/C;
                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                             TFEB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                          MEDLINE=99156862; PubMed=10036191;
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase;
                                                                                                                                                                                                                                                                                                                                     96
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                                                                                                                                                                                                                                                                                                                                                                AGGGTTGTAAGGCATCTCACATTTAC 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 63 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: FIRST ENZYME IN THE N-LINKED OLIGOSACCHARIDE PROCESSING PATHWAY.
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ENDOPLASMIC
                                                                                                                                                                                                                                                                                                                                   rpGlyThrTyrArgProHisValTyr
                                                                                                                                                                                                                                                                                                                                                                                            oValLeuProAlaAspSerSerSerProAlaValAlaProAspLeuPheT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACAT.....
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                                                                                                                                                                                                                                                                                                                                                                                                                        . GTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuAlaTrpTyrArgAlaArgArgAlaValThrLeuHisSerAlaProPr
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                                                                                                                                                                                                                                                                                                       SwissProt_39:TFEB_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       601336;
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657
836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosidase; Glycoprotein; Transmembrane; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCS1_HUMAN
                                                                                                                                                                                                                                                             STANDARD;
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2.130
54.762
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657
91840
                                                                                                                                Chordata;
Rodentia;
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N-LINKED (GLCNAC. ..).
; 57CE4A82126004AC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC
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                                                                                                                              Sciurognathi;
                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                     104
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Identity:
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                                                                                                                                                                                                    update)
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DR (TYPE-II
                                                                                                                                Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42
1
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                                                                                                                                Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
              organization
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alignment_block: US-09-684-016-48411/rev x TFEB_MOUSE
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'GLYCOPROTEIN ZP2) (ZONA PELLUCIDA PROTEIN A) ZP2 OR ZP-2.
                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ZONA PELLUCIDA SPERM-BINDING PROTEIN 2 PRECURSOR (ZONA PELLUCIDA
                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This
          SEQUENCE FROM N.A.,
                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
Transcription regulation; DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF079095; AAD20979.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
TISSUE=Ovary;
                               NCBI_TaxID=10090;
                                                                Mus musculus (Mouse)
                                                                                                                                                P20239;
                                                                                                                                                         ZP2_MOUSE
                                                                                                                                                                                                                                                            106 HisValSer...ProAlaGlnGlySerProLysProAlaProAlaAlaSe 121
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00010; HLH; 1.
SMART; SM00353; HLH; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:103270;
                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001092;
                                                                                                                                                                                                                                       36 TCAGGGTTGTAAGGCATCTCACATTTACAATACC
                                                                                                                                                                                                                                                                                  86 CATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGCCATTAGGTCA
                                                                                                                                                                                                                 rProGlyValArgAlaGlyHisValLeuSerThr 132
                                                                                                                                                                                          SwissProt_39:ZP2_MOUSE
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           AND
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                                           Sciurognathi;
                                                       Craniata; Vertebrata; Euteleostomi;
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                                            Murinae;
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MGD; MGI:99214; Zp2.
InterPro; IPR001507; zona_pellucida.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.

SMART; SM00241; ZP; 1.
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                                                                                                                                           353
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"Oocyte-specific expression of mouse Zp-2: developmental reg
"Oocyte-specific expression of mouse Zp-2: developmental reg
of the zona pellucida genes.";
Mol. Cell. Biol. 10:1507-1515(1990).
-i- FUNCTION: ZP2 FORMS WITH ZP1 AND ZP3 THE ZONA PELLUCIDA,
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TTTATTCCACACAA 12:
                                                                                           GGGCTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAA 107
                                                                                                                                       CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As
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PTM: PROTEOLYTICALLY CLEAVED AFTER FERTILIZATION, AND THIS MODIFICATION, ALONG WITH PRESUMED CHANGES IN ZP3 MAY PLAY AN IMPORTANT ROLE IN THE POSTFERTILIZATION BLOCK TO POLYSPERMY. PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES
                                                pGlyPheMetAspPhe..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP ZP2 ACTS AS A SECONDARY SPERM RECEPTOR.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR
                                                                                                                                                                                    TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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an email to license@isb-sib.ch).
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Gaps: 2
Identity: ·34.211
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DE INTEGRIN BETA-2 PRECE
DE SUBUNIT).
OS ENGRY MCLAZOS;
GN ITGB2 OR CD18.
OS ENGRY MCLAZOS;
GN ITGB2 OR CD18.
OS BOS TAUTUS (BOVINE):
OC MAMMMALIA; Eutheria; GOC MAMMALIA; Eutheria; GOC MAMMALIA; Eutheria; GOC RELUCIA, Eutheria; GOC RELUCIA, Eutheria; GOC RELUCIA, Eutheria; GOC RELUCIA, Eutheria; GOC RELUCIA, Eutheria; GOC RELUCIA, Eutheria; GOC RECONSTEIN COC AMONG THE MOST CAMALIA; GOC CALVES IN THE 19 CC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST COC GOC AMONG THE MOST CAMACIA; GOC GOC AMONG THE MOST COC GOC AMONG TH
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                                                                                                                                                                                                                           EMBL; M81233; AAA30438.1; -. PIR; JC1121; JC1121.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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20-AUG-2001 (Rel. 40, Last annotation update)
INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION GLYCOPROTEINS LFA-
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IPR002369; Integrin_B.
IPR001169; Integrin_beta_C.
IPR003659; PSI.
                                                                                                      IPR002035; vWFA.
                                                                               integrin_B; 1.
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SMART; SM00327; VWA; 1.

PROSITE; PS00243; INTEGRIN_BETA; 3.

PROSITE; PS00027; EFF_1; UNKNOWN_2.

PROSITE; PS01186; EGF_2; UNKNOWN_2.

Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;

Repeat; Extracellular matrix; Cytoskeleton; Signal; Disease mutation.

Repeat; Extracellular matrix; Cytoskeleton; Signal; Disease mutation.

Repeat; Extracellular matrix; Cytoskeleton; Signal; Disease mutation.

Repeat; Extracellular matrix; Cytoskeleton; Signal; Disease mutation.

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                                                                               CysGlnCysAspProGlyTyrGlnPro...ProLeuCysSerGluCysPr 616
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5903ADF4E8998CEA CRC64;
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Gaps: 1
Identity: 42.105
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alignment_scores:
Quality:
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                                                            Align seg
                                                                                          US-09-684-016-48411/rev x YCZ6_YEAST
                                                                                                                                        Ratio:
Percent Similarity:
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PIR; S19418; S19418.
HSSP; P12251; IPVC.
SGD; S0000703; YCR106W.
InterPro; IPRO01138; Zn2_CY6_fungal.
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
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                                                                                                                                                                                                                            PROSITE: PS00463; ZN2_CY6_FUNGAL_1; 1.

PROSITE: PS500469; ZN2_CY6_FUNGAL_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

DNA_BIND 15 42 ZN(2)-CYS(6), FUNGAL-TYPE.

SEQUENCE 832 AA; 95689 MM; 7DF91D86AF08E4E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P25611;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
PUTATIVE 95.7 KDA TRANSCRIPTIONAL REGU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sonnhammer E.;
"What's in a genome?";
"What's in a genome?";
Nature 358:287-287(1992).
-!- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-!- SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
457 IleValTrpAsnLysTyrLysPheHisValIleLeuSer...LysLeuMe
                              122 GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRESENCE OF A ZN(2)-CYS(6) FUNGAL-TYPE BINUCLEAR CLUSTER MEDLINE=92350247; PubMed=1641000; Bork P., Ouzounis C., Sander C., Scharf M., Schneider R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomycetales;
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grenson M., Jauniaux J.-C., Submitted (MAR-1992) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 130-832 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
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Vliet-Reedijk J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                        documentation_block:
                                DMSS_HAEIN STANDARD; PRT; 205 AA. P45003; Q48049; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) ANAEROBIC DIMETHYL SULFOXIDE REDUCTASE CHAIN REDUCTASE IRON-SULFUR SUBUNIT).
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Haemophilus influenzae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as losa its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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Jones S.J.
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                           DMSB OR HI1046.
                                                                                                                                                                                                                                                                                    116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 156 AA; 1
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Rhabditidae; Pelode
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inae; Caenorhabditis.
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Pasteurellaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Doughert B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Grine C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Wolfer C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                             METAL
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Oxidoreductase;
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EMBL; U26665; AAB06234.1; -.
HSSP; P00198; 1FDN.
TIGR; HI1046; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS (BY SIMILARITY).

-:- COFACTOR: IRON-SULFUR (BY SIMILARITY).

-:- SUBUNIT: THE COMPLEX CONSIST OF THREE SUBUNITS: DMSA, THE REDUCTASE; DMSB, AN ELECTRON TRANSFER PROTEIN, AND DMSC, MEMBRANE ANCHOR PROTEIN (BY SIMILARITY).

-:- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae dimethylsulfoxide reductase complex."
Gene 169:137-138(1996).
-!- FUNCTION: TERMINAL REDUCTASE DURING ANAEROBIC GROWTH ON VARIOUS SULFOXIDE AND N-OXIDE COMPOUNDS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BAGAN / SEROTYPE B;
MEDLINE=96186920; PubMed=8635740;
LOOSMORE S.M., Shortreed J.M., Coleman |
"Sequences of the genes encoding the A,
"Sequences of the genes encoding the A,
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MEDLINE=95350630; PubMed=7542800;
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                                                                                                                                                                                                                                                                                                 InterPro; IPR001450;
Pfam; PF00037; fer4;
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4Fe-4S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _documentation_block:
                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                       G-protein NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meleagris gallopavo (Common turkey).
Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR (VIP-R) (VIP RECEPTOR)
                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; PROSITE; PS00650; G_PROTEIN_RECEP_F2_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Vasoactive intestinal peptide stimulates prolactin mRNA expression in turkey pituitary cells: effects of dopaminergic drugs."; Proc. Soc. Exp. Biol. Med. 212:52-62(1966).
-i- FUNCTION: THIS IS A RECEPTOR FOR VIP. THE ACTIVITY OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96206340; PubMed=8618952; Xu M., Proudman J.A., Pitts G.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS
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                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein.
                             EXTRACELLULAR (POTENTIAL)
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                                                                           CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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5 (POTENTIAL).
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(POTENTIAL).
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seq_documentation_block:
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US-09-684-016-48411/rev x VIPR_MELGA
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20-AUG-2001
TAFAZZIN.
                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFZ_HUMAN
Q16635;
                                                                                                                                                                                                                                                                                                                                                                                                    ---
                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bione S., D'Adamo Toniolo D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel X-linked gene, G4.5. is responsible for Barth syndrome.";
Nat. Genet. 12:385-389(1996).
-!- SUBCELLULAR LOCATION: ISOFORMS WITH HYDROPHOBIC N-TERMINUS ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Skeletal muscle, and Heart; MEDLINE=96224398; PubMed=8630491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAZ OR EFE2 OR G4.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 PheGluSerGlyGluProGluHisCysPheValSerSer.ValGlyCysL
                                                                                                                                                                                                             AND SKELETAL MUSCLE. SOME FORMS APPEAR RESTRICTED TO CARDIAC ANI SKELETAL MUSCLE OR TO LEUKOCYTES.

SKELETAL MUSCLE OR TO LEUKOCYTES.

DOMAIN: THE HYDROPHILIC DOMAIN MAY SERVE AS AN EXPOSED LOOP INTERACTING WITH OTHER PROTEINS.

DISEASE: DEFECTS IN TAZ ARE THE CAUSE OF BARTH SYNDROME (BTHS), SEVERE INHERITED DISORDER, OFTEN FATAL IN CHILDHOOD, CHARACTERIS SEVERE INHERITED DISORDER, OFTEN FATAL IN CHILDHOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                    THOUGHT TO BE MEMBRANE ANCHORED. SHORTEST FORMS, LACKING THE HYDOPHOBIC STRETCH, MAY BE SOLUBLE FOR TOPLASMIC PROTEINS.

ALTERNATIVE PRODUCTS: UP TO 10 ISOFORMS. SHORTER TAPAZZINS START WITH THE SECOND METHIONINE AT POS. 25. ALTERNATIVE SPLICING OF THE HYDROPHILIC CENTRAL REGION (EXONS 5-7) MAY PRODUCE 5 VARIANTS. TWO ISOFORMS, CONTAINING ALL THREE EXONS OR LACKING EXON 5 ONLY ARE CONSISTANTLY ABUNDANT. THE SEQUENCE SHOWN HERE IS THAT OF THE
                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY: HIGH LEVELS IN CARDIAC AND SKELETAL MUSCLE. UP TO 10 ISOFORMS CAN BE PRESENT IN DIFFERENT AMOUNTS IN DIFFERENT TISSUES. MOST ISOFORMS ARE UBIQUITOUS. ISOFORMS THAT LACK THE N-TERMINUS ARE FOUND IN LEUKOCYTES AND FIBROBLASTS, BUT NOT IN HEART
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                                                                                                                                                                                                 BY CARDIAC AND SKELETAL MYOPATHY, SHORT STATURE AND NEUTROPENIA.
                                                                                                                                                                                                                                                                                                                                                                                                                         LONGEST ISOFORM.
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InterPro; IPR000872; Tafazzin.
Pfam; Pf01553; Acyltransferase; 1.
PRINTS; PR00979; TAFAZZIN.
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MOST OF THE ENERGY REQUIRED FOR TRANSPORT PROCESSES VACUOLAR SYSTEM.

VACUOLAR SYSTEM.

SUBUNIT: V-AATPASE IS AN HETEROMULTIMERIC ENZYME COMFERSIPHERAL CATALYTIC VI COMPLEX (COMPONENTS A TO H)

AN INTEGRAL MEMBRANE VO PROTON PORE COMPLEX (COMPONE
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                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                              "Absence of mutations involving the gene LHX9 in 46,XY gagenesis and dysgenesis.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN GONADAL DEVELOPMENT (BY SIMILA-
-i- SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
-i- SUBLIBARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9NQ59; Q9NQ70;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIM/HOMEOBOX PROTEIN LHX9.
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InterPro; IPR002843; VATP-Synt_AC39.
Pfam; PF01992; VATP-Synt_AC39; 1.
Hydrolase; Hydrogen ion transport.
SEQUENCE 348 AA; 39596 MW; 016BI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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-!- SIMILARITY: BELONGS TO THE V-ATPASE VOD/AC39 SUBUNIT FAMILY.
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Gaps:
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US-09-684-016-48411/rev x LHX9_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: SwissProt_39:LHX9_MOUSE
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Pfam; PF000412; LIM; 3.
ProDom; PD000094; LIM; 2.
SMART; SM00389; HOX; 1.
SMART; SM00382; LIM; 2.
PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50027; HOMEOBOX_1; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
PROSITE; PS00027; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AJ277916; CAB98128.1; ALT_SEO.
EMBL; AJ277917; CAB98128.1; JOINED.
EMBL; AJ277918; CAB98128.1; JOINED.
EMBL; AJ277919; CAB98128.1; JOINED.
EMBL; AJ277919; CAB98128.1; JOINED.
EMBL; AJ277920; CAB98128.1; JOINED.
InterPro; IPRO01356; Homeobox.
InterPro; IPRO01781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metal-binding; Z
DOMAIN 62
DOMAIN 124
DNA_BIND 258
SEQUENCE 388 A
                                                                                                                                                                                                                               LHX9_MOUSE STANDARD; PRT; 388 AA.
09WUH2; O9WU44; Q9QYQ5; Q9QXQ0;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
LIM/HOMEOBOX PROTEIN LHX9.
                                                                                                                                                                                                                                                                                                           documentation_block:
STRAIN-NIH SWISS;
MEDLINE-99264291; PubMed=10330499;
Bertuzzi S., Porter F.D., Pitts A.,
                                                                           MEDLINE=99098964; PubMed=9880598;
Retaux S., Rogard M., Bach I., Failli V.,
"Lhx9: a novel LIM-homeodomain gene expres
forebrain.";
                                                                                                                               SEQUENCE OF 1-300 FROM N.A. STRAIN=C57BL/6;
                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                       SEQUENCE OF 11-388 FROM N.A.
                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                       LHX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homeobox; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires
                                                                                                                                                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                   Neurosci.
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Ratio:
Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TATCACCTTACATGTGAAACTTACCAGTCAGTGCAGCCCTCGCATTGCGC
                                                                                                                                                                                                                                                                                                                                                             hrGlyAspHisPheGlyMetLysAspSerLeuValTyr 173
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email to license@isb-sib.ch).
                                                                 19:783-793(1999)
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Rodentia;
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A4DC8B914D7C3B66
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Sciurognathi; Muridae;
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 Kumar M.,
                                                                                       li V., Besson expressed in
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40.000
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 Agulnick A., Wassif C.,
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                                                                                       M.J.;
the developing
                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain;
                                                                                                                                                                               Murinae; Mus
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    Quality:
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                                                                                                                                                                                                                                              PROSITE; PS00478; LIM_DOMAIN_1; 2.
PROSITE; PS50023; LIM_DOMAIN_2; 2.
HOMEOBOX; DNA-binding; Nuclear protein; Repumetal-binding; Zinc; Alternative splicing.
Metal-binding; Zinc; Alternative 1: LIM 1.
DOWAIN 62 114 LIM 2.
DOMAIN 124 177 LIM 2.
DNA_BIND 258 317 HOMEOBOX.
VARSPLIC 304 388 VAFONARAKERRNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001781; LIM.
Pfam; PF00046; homeobox; 1.
Pfam; PF000412; LIM; 2.
ProDom; PD000094; LIM; 2.
SMART; SM00139; HOX; 1.
SMART; SM00132; LIM; 2.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS00071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF134761; AAD30110.1; -.
EMBL; AF13518; AAD22008.1; -.
EMBL; AAZ43851; CAB59907.1; -.
EMBL; AJ243852; CAB59908.1; JOINI
EMBL; AJ243853; CAB59908.1; JOINI
EMBL; AJ243853; CAB59908.1; JOINI
EMBL; AJ243855; CAB59908.1; JOINI
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EMBL; AJ243857; CAB5909.1; JOINI
EMBL; AJ243857; CAB5909.1; JOINI
                                                                                               CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001356; Homeobox. InterPro; IPR001781; LIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1316721; Lhx9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20221375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND ALTERNATIVE
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153
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VWFQNARAKFRRNLLRQENGGVDKADGTSLPAPPSADSGAL
TPPGTATTLTDLTNPTVTVTTVISNADSHEPGSPSOTTLT
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cerebral cortex.";
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-> F (IN REF. 2).
C2D7326A68D87B32
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Ratio: Percent Similarity:

48.00 2.824 56.667

Length: Gaps: Percent Identity:

30 1 40.000

alignment_block:

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seq_name:
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                                                                                           InterPro; IPR000488; Death.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR_NGFR_1; 3.
PROSITE; PS0065; TNFR_NGFR_1; 3.
PROSITE; PS0065; TNFR_NGFR_2; 3.
PROSITE; PS0017; DEATH_DOMAIN; 1.
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NGFR_CHICK STANDARD;
 DOMAIN
TRANSMEM
DOMAIN
                                                          Phosphorylation;
SIGNAL 1
                                                                                                                                                                                                    PIR; JN0006; JN0006.
PIR; A60504; A60504.
HSSP; P07174; INGR.
                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 21-416 FROM N.A.

MEDILINE-90152140; PubMed=2154393;

Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell

"Structure and developmental expression of the chicken

Dev. Biol. 137:287-304(1990).

-!- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO
                                                CHAIN
                                                                                                                                                                                                                                          ++++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P18519;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Large T.H., Weskamp G., Helde Shooter E.M., Reichardt L.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                             Neuron 2:1123-1134(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                       "Structure and developmental expression receptor in the chicken central nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90166579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GP80-LNGFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOW-AFFINITY NERVE
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SUBUNIT: NGF RECEPTOR
BOND FORMATION.
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                                                                                   Neurogenesis;
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262
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                                                                    Signal.
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mp G., Helder J.C.,
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 239
261
416
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                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                   CAN FORM
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LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION
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                                  POTENTIAL.
LOW-AFFINITY
RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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                                                                                  Glycoprotein;
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                                               GROWTH
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                                                                                  Repeat;
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                                                                                                                                                                                                                                                                                                                                                 NGF
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                                                                                                                                                                                                                                                                                                   DISULFIDE
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SEQUENCE FROM N.A.
MEDLINE=87115859; PubMed=3027580;
Radeke M.J., Misko T.P., Hsu C., Herza
Radeke M.J. Misko T.P., Hsu C., Herza
Radeke M.J. Misko T.P., Hsu C., Herza
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Radeke M.J., Misko T.P., Hsu C., 
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Metsis M., '
                                                     TISSUE-Liver;
MEDLINE=93077038; PubMed=1446821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (I
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
                                                                                                                              SEQUENCE OF 1-22
                                                                                                                                                                                                 Nature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SwissProt_39:NGFR_RAT
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                                 Timmusk
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)a; Chordata;
.a; Rodentia;
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                              Allikmets
llikmets R., Saarma
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Cook E.H. Jr.;
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seq_name: SwissProt_39:GAC3_HUMAN
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EMBL;
                              use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O99928; O9HD46; Q9NYT2;
15-JUL-1998 (Rel. 36, Created)
20-AUG-2001 (Rel. 40, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA
                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/
-i- FUNCTION: GABA, THE MAJOR INI
-i- FUNCTION: GABA, MEDIATES NE
GABA/BENZODIAZEPINE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                  Han M.K., Chen Y.-H.
"Gene structure and
(GABRG3) gene.";
                                                                                                                                                                                                                                                                                                                                                                                                              gamma 3 subunits.";
Eur. J. Pharmacol.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                 "Genomic organization of GABAA receptor gamma (GABRG3).";
                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 19-467
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MEDLINE=96360042; PubMed=8719414;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression and pharmacology of human GABAA receptors containing
                                                                              s SWISS-PROT entry is copyright. It is produ
ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
                                                                                                                                                                  SUBUNIT: GENERALLY PENTAMERIC. THERE ARE RECEPTOR CHAINS: ALPHA, BETA, GAMMA, DEI SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
                                                                                                                                                       MISCELLANEOUS: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysArgCysAlaTyrGlyTyrTyrGlnAspGluGluThrGlyHisCysGl 124
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            S82769; AAB39369
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Metazoa; Chordata; C
Metazoa; Primates; (
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alignment_block:
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CARBOHYD
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CONFLICT
SEQUENCE
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                      MM17_HUMAN STANDARD; PRT; 606 AA.
Q9UL29; Q14850;
20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
20-AUG-2001 (Rel. 40, Last annotation update)
MATRIX METALLOPROTEINASE-17 PRECURSOR (EC 3.4.24.-)
(MEMBRANE-TYPE MATRIX METALLOPROTEINASE 4) (MT-MMP 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro: IPR001175; Neur_chan Pfam; PF00065; neur_chan; 1. PRINTS; PR00252; NRIONCHANNEL. PRINTS; PR00253; GABAARECEPTR.
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        MATRIX METALLOPROTEINASE)
MMP17 OR MT4MMP.
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EMBL;
Homo
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                                                                                                                           aGluCysGlnLeuGlnLeuHisAsnPheProMetAspGluHisSerCys
                                                                                                                                             TCAGTGCAGCCCTCGCATT....
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sapiens
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AF269143
AF228458
AF228458
AF228451
AF228451
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CYTOPLASMIC (PROBABLE).
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type 4 ma
J. Biol.
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-!- CATALYTIC ACTIVITY: CLEAVES PRO-TNF-ALPHA AT THE 74-ALA-|-GLN-75 SITE.

-!- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY (BY SIMILARITY).

-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A GUIDEN CARE TO THE MEMBRANE BY A GRITANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 matrix metalloproteinase.";
Biol. Chem. 380:1103-1108(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20036570; PubMed=10567400; Itoh Y., Kajita M., Kinoh H., Mori H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang Y., Johnson A.R., Ye Q.~Z., Dyer R.D.; "Catalytic activities and substrate specificity of the type 4 matrix metalloproteinase catalytic domain."; J. Biol. Chem. 274:33043-33049(1999).
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MEDLINE=96234364; PubMed=8640782;
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                                                                                                                                                                                                                                                                                             -! - PTM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20008793; PubMed=10543448;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                 SIMILARITY).

SIMILARITY: CONTAINS 1 HEMOPEXIN-LIKE DOMAIN.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY MIDA (ZINC METALLOPROTEASE) ALSO KNOWN AS MATRIXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                    SHORT/PUENTE-TYPE FORM; ARE PRODÜCED BY ALTERNATIVE SPLICÎNG. TISSUE SPECIFICITY: EXPRESSED IN BRAIN, LEUKOCYTES, COLON, OV TESTIS AND BREAST CANCER. EXPRESSED ALSO IN MANY TRANSFORMED NON-TRANSFORMED CELL TYPES.
                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                             THE PRECURSOR IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcript: isolation of complementary DNA clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ., Will H.; catalytic domain
                                There are no restrictions in as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seiki M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okada
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                                                                                              EMBL outstation
                                                                                                                     a collaboration
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in no way
commercial
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

MIM; 602285;

Hemopexin.

м10.017; -.

X89576; CAA61753.1; P08254; 1USN. AB021225; BAA82707.1;

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seq_documentation_block:
ID APC2_CAVPO STANDA
AC P27916;
DT 01-AUG-1992 (Rel. 23,
DT 01-AUG-1992 (Rel. 23,
DT 01-NOV-1995 (Rel. 32,
DT 01-NOV-1995 (Rel. 32,
DE APOLIPOPROTEIN C-II P
GN APOC2.
OS Cavia porcellus (Guin
                                                                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
Ratio:
                                                                                                       seq_name: SwissProt_39:APC2_CAVPO
                                                                                                                                                                                                                                                                            alignment_block:
US-09-684-016-48411/rev x mm17_HUMAN
                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: MM17_HUMAN
                                                                                                                                                                                                                                                                                                            Percent Similarity:
                  P27916;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
APOLIPOPROTEIN C-II PRECURSOR (APO-CII)
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CONFLICT
SEQUENCE
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROPEP
CHAIN
PROPEP
DOMAIN
 Cavia porcellus (Guinea pig).
                                                                                                                              163
                                                                                                                                                                                                                                     116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000130; Zn_MTpeptds
Pfam; PF00045; hemopexin; 4.
Pfam; PF00413; Peptidase_M10; 1.
                                                                                                                                                                       146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00142; ZINC_PROTEASE; 1.
PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00120; HX; 4.
SMART; SM00235; ZNMC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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GPI-anchor; Extracellular matrix; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000585;
InterPro; IPR001818;
                                                                                                                                                                                           66
                                                                                                                                                                                  TGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTACCAGTCA
                                                                                                                             etTyrTyr 165
                                                                                                                                                  ACATTTAC 9
                                                                                                                                                                     gThrPheProArgAspSerProLeuGlyHisAspThrValArgAlaLeuM 163
                                                                                                                                                                                                               129
569
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113
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N-LINKED (GLCNAC. ..) (POTENT
MISSING (IN SHORT ISOFORM).
GPGGTV -> ARRHR (IN REF. 1).
D -> Y (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYSTEINE SWITCH (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MATRIX METALLOPROTEINASE-17
REMOVED IN MATURE FORM (POT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HEMOPEXIN-LIKE.
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                            -> N (IN REF. 1).
F3BF2EF21918F44C CRC64;
                                                                                                                                                                                                                                                                                                           Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CATALYTIC)
                                                                                                                                                                                                                                                         to:
                                                                                                                                                                                                                                                                                                                                 Length:
                                                                          100
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                                 update)
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1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
TISSUE=Embryo;
TISSUE=Embryo;
MEDLINE=95220383; PubMed=7705369;
Yamasu K., Watanabe H., Kohchi C., Soma G.-I., Mizuno D.-I.,
Yamasu K., Shimada H., Suyemitsu T., Ishihara K.;
Akasaka K., Shimada H., Suyemitsu T., Ishihara K.;
"Molecular cloning of a cDNA that encodes the precursor to several
"Molecular cloning of peptides, epidermal-growth-factor-related
                                                                                                                                                                                                                                                                                                                                                                                              EGIP_ANTCR STANDARD; PRT; 325 AA.

P15217; P15218; P15219;
01-APR-1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
EXOCASTRULA-INDUCING POLYPEPTIDE PRECURSOR (EGIP).
Anthocidaris crassispina (Sea urchin).
Enkaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                Anthocidaris.
NCBI_TaxID=7629;
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J. Biol. Chem. 266:4074-4080(1991).

-i- FUNCTION: APOC-II IS A COMPONENT OF THE VERY LOW DENSITY

-i- FUNCTION: APOC-II TA COMPONENT OF THE VERY LOW ACTIVATOR OF

ELPOPROTEIN (VLDL) FRACTION IN PLASMA, AND IS AN ACTIVATOR OF

SEVERAL TRIACYLGIZCEROL LIPASES. THE ASSOCIATION OF APOC-IN WITH

PLASMA CHYLOMICRONS, VLDL, AND HDL IS REVERSIBLE, A FUNCTION OF

THE SECRETION AND CATABOLISM OF TRIGLYCERIDE-RICH LIPOPROTEINS,
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   Echinoidea; Euechinoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=91154195; PubMed=1999402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M59913; AAA37031.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                          Echinacea;
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PROSITE: PS00022; EGF_1; FALSE_NEG.

PROSITE: PS00022; EGF_1; FALSE_NEG.
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SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochim. Biophys. Acta 999:24-28(1989).

-I. FUNCTION: THE EGIP PEPTIDES ARE FACTORS EFFECTIVE TO EXTRUDE TARCHENTERON TOWARD OUTSIDE OF EMBRYOS. MAY HAVE A ROLE IN THE INDUCTION OF GASTRULATION.

-I. SIMILARITY: EACH OF THE 4 PEPTIDES CONTAINS 1 EGF-LIKE DOMAIN.
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PIR; A48167; A48167.
PIR; B48167; B48167.
PIR; S06637; S06637.
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Eur. J. Bioch
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SM00001; EGF_like;
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BY SIMILARITY.

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sp_human:Q9Y6N4
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Query length: 123
Database: SPTREMBL_17:*
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sp_invertebrate:Q44498
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-Q-/cgn2_1/USPTO_spool/US09684016/runat_19032002_084440_20931/app_query.fasta_1.182
-Q-/cgn2_1/USPTO_spool/US09684016/runat_19032002_084440_20931/app_query.fasta_1.182
-DB=SPTREMBL_17-OFMT-fastan -SUFFIX=std.rspt -GAPOP=12.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-OGAPEXT=0.100 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -FGAPEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -NINLEN=0 -MATRIX=D0000000
-USER=US09684016_@CGN1_1_96 -NCPU=6 -ICPU=3 -LONGLOG
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27 i 043479 hordeum vulgare (barley)

28 i 09fen9 arabidopsis thaliana (mc)

28 i 09svi4 arabidopsis thaliana (mc)

29 i 09svi4 arabidopsis thaliana (mc)
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5 | Q4u498 caenorhabditis elegan
6 | Q4u708 drosophila melanogast
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sp_virus:Q98VX5 +
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seq_documentation_block:
ID 065462
AC 065462;
AC 065462;
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AC 065462;
AC 065462;
AC 01-AUG-1998 (TrEMBLrel. 07)
DT 01-AUG-1998 (TREMBLrel. 17)
DE RECEPTOR LIKE PROTEIN (FRAMELY)
AC 01-JUN-2001 (TREMBLRel. 17)
DE RECEPTOR LIKE PROTEIN (FRAMELY)
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC ENARYOTA; Viridiplantae;
AC NCBLTAXID-3702;
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Pfam; PF00628; PHD; 1.
SMART; SM00439; BAH; 1.
SMART; SM00249; PHD; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 201 AA; 22979 MW; 4C48
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RECEPTOR LIKE PROTEIN (FRAGMENT).
F1N20.240 OR AT4G22140.
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EU Arabidopsis sequencing project;
EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL022140; CAA18117.1; -.
EMBL; AL161556; CAB79169.1; -.
EMBL; AL161556; CAB79169.1; -.
EMBL; AL161556; CAB79169.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
131 sGluGlyCysLysAspTrp
                                                                                                                    115 TyrCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy
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InterPro; IPR000561; EGF-like
InterPro; IPR001965; PHD.
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Robben J., Grymonprez B., Volckaert G, Mewes H.W., Lemcke
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Q9fk65 arabidopsis thaliana
! Q9vg78 drosophila melano
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Q43479 PRELIMINARY;
Q43479; Crembtrel. 0:
01-NOV-1996 (Trembtrel. 0:
01-NOV-2001 (Trembtrel. 1:
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                                                                                                                                                    Q9FEN9;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation
PUTATIVE PHD FINGER TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                     _documentation_block:
         Oh M., Torisky R.S., Braam J., Altmann T., Clo
"PHD Finger Dependent Binding of SHL1 to a Spe
Arabidopsis TCH4 in vitro.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF277453; AAG21353.1;
InterPro; IPR001025; BAH.
                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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SMART; SM00249; PHD;
SEQUENCE 227 AA;
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InterPro; IPR000561; EGF-like.
InterPro; IPR001025; BAH.
InterPro; IPR001965; PHD.
Pfam. BERGERO
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Pfam; PF01426; BAH; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
 InterPro;
                                                                            SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=3702;
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Triticeae; Hordeum.
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T 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
T 01-UN-2001 (TrEMBLrel. 17, Last annotation update)
E ES43 LIKE PROTEIN (FRAGMENT).

N F19H22.200 OR AT4G39100.
S Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tray
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
curosids II; Brassicales; Brassicaceae; Arabidopsis.
(NCBL_TaxID=3702;
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BEVAN M., Murphy G., Ridle

Bevan M., Schueller C

Mayer K.F.X., Schueller C
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Pfam; PF01426; BAH; 1.
Pfam; PF00628; PHD; 1.
SMART; SM00439; BAH; 1.
SMART; SM00249; PHD; 1.
PR051TE; PS00322; H1ST0NE_H3_1; UJ
SEQUENCE 228 AA; 26122 MW; A80
InterPro; IPR001
Pfam; PF01426; B
Pfam; PF00628; P
SMART; SM00439;
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Q9SVI4 PRELIMINARY;
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                                                                               EU Arabidopsis sequencing projections of the EM Submitted (MAR-2000) to the EMBL; AL035679; CAB38830 1; --
EMBL; AL161594; CAB80573.1; --
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Smith A., 1
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                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                 , Ridley P., (MAR-2000) t
                                                                                                                                                       Mewes H.W., Lemcke K., Mayer K.F.X.; (MAR-2000) to the EMBL/GenBank/DDBJ
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Percent Identity:
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CHINESE SPRING; TISSUE-ROOT;
Nemoto Y., Kawakami N., Sasakuma T.;
"Isolation of novel early salt-responding genestivum L.) by differential display.";
Theor. Appl. Genet. 98:673-678(1999).
EMBL; AB011445; BAA82157.1; -.
InterPro; IPR001965; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
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    Q9xJ51 PRELIMINARY;
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01-NOV-1999
01-JUN-2001
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00249; PHD; 1.
PROSITE; PS01186; EGF_2; UNKNOWN
PROSITE; PS00322; HISTONE_H3_1;
NON_TER 258 258
SEQUENCE 258 AA; 29675 MW; 1
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17 p 17
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(TrEMBLrel. 17,
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seq_name: sp_human:Q9Y6N4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
SEQUENCE FROM N.A.

MEDLINE=99160472; PubMed=10051327;

Hasenpusch-Theil K., Chadwick B.P., Theil

Wilkinson D.G., Frischauf A.M.;

"PHF2, a novel PHD finger gene located or

Mamm. Genome 10:294-298(1999).

EMBL; AF043725; AAD21791.1;

InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                documentation_block:
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                                                                                                              Homo sapiens (Human).
Homo sapiens (Human).
'--rvota; Metazoa; Chordata; f
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Q9Y6N4;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TREMBLrel. 17,
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InterPro; IPR001965; pHD.
Pfam; pF00628; PHD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
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O9WTU0;

O1-NOV-1999 (TrEMBLrel. 12,

O1-NOV-1999 (TrEMBLrel. 12,

O1-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wilkinson D.G., Frischauf A.M.;
"PHF2, a novel PHD finger gene located on
Mamm. Genome 10:294-298(1999).
EMBL; AF043726; AAD21792.1; -.
MGD; MGI:1338034; Phf2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                         PHD-FINGER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Hasenpusch-Theil K., Chadwick B.P.
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                                                                                                                                                                                                                                                                                                                     CGAGGGCTGCACTGACTGG 73
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InterPro; IPR001965; PHD
Pfam; PF00628; PHD; 1.
PROSITE; PS01186; EGF_2;

EGF_2; UNKNOWN_1.

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RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Apbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Melson D.R., Nelson K.A., Nixon K., Nuxskern D.R., Nelson D.L.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
            TRANSPARATA
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Q9VJE3;

Q1-MAY-2000 (TrEMBLrel. 1

01-MAY-2000 (TREMBLrel. 1

01-JUN-2001 (TREMBLrel. 1

CG15141 PROTEIN.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea; Drosophilidae; Drosophila.
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73.913
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121063 MW; DA1AD9826FFF3B77 CRC64;
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Gaps: 0
Percent Identity: 43.478
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Last annotation update)
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q. Zheng L.,
RA Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhou W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Wyers E.W., Rubin G.M., Venter J.C.;
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Science 287:2185-2195(2000).
DR EMBL; AE003655; AAF33607.1; -.
DR F1yBase; FB9n003263; CG15141.
DR InterPro; IPR001126; ZhF UBR1.
DR InterPro; IPR003126; ZhF UBR1.
DR Ffam: PP02207; Zf-UBR1; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
Q9HAH2 PRELIMINARY;
                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ11634 FIS, CLONE HEMBA1004275, MODERATELY SIMILAR TO HOMO
SAPIENS PHD-FINGER PROTEIN (GRC5) MRNA (FRAGMENT).
                PROSITE; PS01186; EGF_2; UNKNOWN_1.
NON_TER 790 790
                                           Pfam; PF00628; PHD; 1
SMART; SM00249; PHD;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-WHOLE EMBRYO,
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 uValMetLeuGlnCysAlaIleCysGluAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 TyrCysLysCysLysArgProTyrProAspProAspArgThrValGluGl 161
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                       InterPro; IPR000561; EGF-like.
InterPro; IPR001965; PHD.
                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                           Eutheria; Primates; Catarrhini; Hominidae;
 790 AA;
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4.250
64.286
 88642 MW; D4D21D2A766C671A CRC64;
                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
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SQ TERM
seq_documentation_block
                     seq_name:
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US-09-684-016-48411 x Q9UPP1
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Quality:
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MEDLINE=99397452; .

Kikuno R., Nagase T., Isi...

Tanaka A., Kotani H., Nomura N., ...

f "Prediction of the coding sequences of

The complete sequences of 100 new cDNP

RT for large proteins in vitro.";

DNA Res. 6:197-205(1999).

"DNA Res. 6:197-205(1999).

"DNA Res. 6:197-305(1999).

"AG61; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: sp_human:Q9UPP:
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US-09-684-016-48411 x Q9HAH2
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Q9UPP1 PRELIMINARY;
                                                                                                                                                                                                                                                                                                   Pfam; PF PROSITE;
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                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                          SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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Similarity:
                                                                                        TyrCysLeuCysArgLeuProTyrAspValThrArgPheMetIleGluCy
                                                                                                               TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                           sAspMetCysGlnAspTrp
                                                                   CGAGGGCTGCACTGACTGG
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                    sp_fungi:Q03012
                                                                                                                                      1/1
                                                                                                                                                                                                                                                                                                 PF00628; PHD; 1.
TE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                          SM00249;
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                                                                                                                                                                                                                                                                    1084
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4.625
69.565
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4.625
69.565
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Primates;
                                                                                                                                                                                                                                                                   120376 MW;
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Nomura N., Ohara O.;
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Gaps: 0
Percent Identity: 43.478
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Gaps: 0
Identity: 43.478
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RX MEDLINE-9731371; PubMed-9169875;
RX MEDLINE-9731371; PubMed-9169875;
RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,
RA Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Churcher C., Coster F., Davis K., Davis R.W., Dietrich F.S.,
RA Delius H., DiPaolo T., Dubois E., Dusterboft A., Duncan M., Floeth M.,
RA Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,
RA Heumann K., Hilbert H., Hiller L., Hunlcke-Smith S., Hyman R.,
RA Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,
RA Lew H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,
RA Mewes H.W., Mirtipati S., Moestl D., Marathe R., Messenguy F.,
RA Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,
RA Nentwich U., Schafer M., Scharens B., Schramm S.,
RA Purnelle D., Schafer M., Scharens B., Schramm S.,
RA Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,
RA Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q03012;
Q03012;
Q1-NOV-1996
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                               adrenoleukodystrophy gene.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95320205; PubMed=7597071;
Shani N., Watkins P.A., Valle D.;
"PXA1, a possible Saccharomyces cerevisiae ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A new family of yeast genes implicated in ergosterol synthesis is related to the human oxysterol binding protein."; reast 10:341-353(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activated protein kinase-kinase homologs, mediated by protein kinase C."; Mol. Cell. Biol. 13:3076-3083(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93140769; PubMed=8423796;
Brigati C., Kurtz S., Balderes D., V
"An essential yeast gene encoding a '
Mol. Cell. Biol. 13:1306-1314(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tzagoloff A., Capitanio N., Nobrega M.P., Gatti D.; "Cytochrome oxidase assembly in yeast requires the phomolog of the P. denitrificans protein encoded by EMBO J. 9:2759-2764(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPI8P
                             Swartzman
                                           SEQUENCE FROM N.A.
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                                                                          "The nucleotide se
Nature 387:0-0(0).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPL138C OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Irie K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and MKK2, which encode Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takase
           E., Viswani
(APR-1996)
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                            Viswanathan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X
                                                                                         sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=8386320;
., Lee K.S., Levin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomycetaceae;
             ţ
             the EMBI
                                                                                         of
             .N., Emerick A.E., EMBL/GenBank/DDBJ
                                                                                         Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                               92:6012-6016(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vidali G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.E., Araki H., Matsumoto K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces
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function in the path
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repeat-binding
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             Thorner J.; databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product of COX11, a
ORF3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               of.
                                                                                         chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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alignment_scores:
    Quality:
    Ratio:
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    Quality:
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Percent Similarity:
alignment_block:
US-09-684-016-48411 x 074508
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_fung1:074508
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                                                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
074508 PRELIMINARY;
                                                                                                                         Rieger M., Lyne M., Rajandream M.A., Barrell B.G.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031523; CAA20664.1; -.
Interpro; IPR001965; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                 074508
074508;
                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetas;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TremBLrel. 08, Created)
01-NOV-1998 (TremBLrel. 08, Last sequence update)
01-UN-2001 (TremBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN, PHD FINGER CONTAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jia Y., Cherry J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases EMBL; U43703; AAB68222.1; -.
SGD; S0006059; YPLI38C.
                                                                                                                                                                                                                                                                                                                SPCC594.05C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001965; PHD. Pfam; PF00628; PHD; 1. SMART; SM00249; PHD; 1. SEQUENCE 353 AA; 41468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Storms R.K., Vo D.H.,
Submitted (APR-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A Hall J., DePaulo Storms R.K., Vo I
                                                                                                                                                                                                             STRAIN-972H-;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [01]
                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CGAGGGCTGCACTGACTGG
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                                                                                                                  AA;
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AA; 41468 MW;
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4.156
69.565
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4.167
60.000
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                                                                                                                    48683
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Gaps:
Percent Identity:
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                                                                                                                    2963605C3DFCC0B9 CRC64;
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                                    Identity:
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Gaps:
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47.826
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alignment_block:
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ID 045410 PRELIMINARY;
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                                                                  Align seg 1/1 to: 045410 from: 1
                                                                                                      US-09-684-016-48411 x 045410
                                                                                                                                                          Percent Similarity:
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045410;
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
172 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
                                                                                                                                                                                                                                                         SMART; SM00297; BROMO;
SMART; SM00249; PHD; 2
SEQUENCE 405 AA; 46
                                                                                                                                                                                                                                                                                                            PRINTS; PRO0503; BROMODOMAIN.2; 1. PROSITE; PS50014; BROMODOMAIN.2; 1. PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 GCAATGCGAGGGCTGCACTGACTGG
|||:::||||||
| 133 uGlyCysAspGlyCysGluAspTrp
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 2.
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z81515; CAB04198.1; -
Interpro; IPR000561; EGF-like.
Interpro; IPR001487; Bromodomain.
Interpro; IPR001965; PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barlow K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
                              5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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                                                                                                                                                                        Quality:
Ratio:
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34.783
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CGAGGGCTGCACTGACTGG

seq_name:

sp_invertebrate: Q9NLC1

PRT;

451

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seq_documentation_block:
ID Q9NLC1;
AC Q9NLC1;
DT Q1-CCT-2000 (TTEMBLTel. 15
DT Q1-CCT-2001 (TTEMBLTel. 15
DT Q1-CCT-2001 (TTEMBLTel. 15
DT Q1-CCT-2001 (TTEMBLTel. 17
DE F26H11.3C PROTEIN.
GN F26H11.3C.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemato.
OC Rhabditidae; Peloderinae; (OR NCBLTAXID-6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the RN [2]
RN ESQUENCE FROM N.A.
RA Barlow K.;
RL Submitted (NOV-1996) to the RN [2]
RN ESQUENCE FROM N.A.
RA Barlow K.;
RI SUBMITTE SPOOS613; PUDMed-9)
RA none; Sequence of the new Sequence 282:2012-2018(1998)
RN INTERPO, IPRO01487; BGF-1
DR INTERPO; IPRO01487; BGF-1
DR INTERPO; IPRO01487; BGF-1
DR FAMBL; SMOR297; BROMODOMA:
DR PANTTS; PRO0523; BROMOODA:
DR PANTTS; PRO0523; BGF-2
DR PROSITE; PS01186; EGF-2
DR SEQUENCE 451 AA; 52035 1
   AC DT DT DT OC OC OC
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01-JUN-1998 (TrEMBLrel. 0
01-JUN-2001 (TrEMBLrel. 1
F26H11.3B PROTEIN.
F26H11.3B.
                                                                                                                                                                                                                                                                                                                       _documentation_block:
O45407 PRELIMINARY;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                      045407;
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PROSITE; PS01186; EGF_2; UNKNOWN_1.
SEQUENCE 451 AA; 52035 MW; 349F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 282:2012-2018(1998).
EMBL; 281515; CAB54234.2; -.
                                                                     Caenorhabditis elegans.
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IPR000561; EGF-like.
IPR001965; PHD.
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Last annotation update)
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seq_documentation_block:
ID Q9UIG2
AC Q9UIG2;
AC Q9UIG2;
AT Q1-MAY-2000 (TrEMBLrel. 13
DT Q1-MAY-2000 (TrEMBLrel. 13
DT Q1-JUN-2001 (TrEMBLrel. 17
DE BROMODOMAIN PHD FINGER TRA
GN BPTF.
QS Homo sapiens (Human).
QC Eukaryota; Metazoa; Chorda
QC Eukaryota; Metazoa; Chorda
QC Mammalia; Eutheria; Primat
QX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
Jones M.H., Hamana N., Shi
RA Jones M.H., Hamana Ocharc'
RT Transcription factor.";
RL Submitted (SEP-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00503; BROMODOMAIN.
PROSITE; PS50014; BROMODOMAIN_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
SMART; SM00297; BROMO; 1.
SMART; SM00299; PHD; 2.
CECUTAGE ETO 25. E7000 M3. CF67
                                      SEQUENCE FROM N.A.

Jones M.H., Hamana N., Shimane M.;

"Iedentification and charcterization BPTF a novel bromodomain
                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BROMODOMAIN PHD FINGER TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 TyrCysValCysGlnLysProTyrAspAspThrLysPheTyrValGlyCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00439; bromodomain; 1. Pfam; PF00628; PHD; 2.
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                                                                                                                                                                                                                                                                                                                                                                                              293
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InterPro; IPR001487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
EMBL; Z81515; CAB04195.1;
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                                                                                                                                Chordata;
Primates;
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     to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                              299
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                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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US-09-684-016-48411 x Q9UIG2
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Quality:
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EMBL; AF010404; AAC51735.1; -.
InterPro; IPR000910; HMG_12_box.
InterPro; IPR001214; SET:
InterPro; IPR001822; Recombinase.
InterPro; IPR001955; PHD.
InterPro; IPR002965; P-grich_extensn.
InterPro; IPR003616; PostSET:
InterPro; IPR003888; FYrich_N.
InterPro; IPR003888; FYrich_C.
Deface: DEF06280; DEF0.
Pfam: PF00628; PHD; 3.
Pfam: PF00856; SET; 1.
PRINTS: PR01217; PRICHENTENSN.
PROSITE: PS00398; RECOMBINASES_2; UI
PROSITE: PS50280; SET; 2.
SMART: SM00541; FYRC; 1.
SMART; SM00541; FYRN; 1.
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O14687 PRELIMINARY;
O14687;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLIND=97388474; PubMed=9247308;
Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,
Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00297; BROMO; 1.
SMART; SM00249; PHD; 2.
SEQUENCE 2781 AA; 311210 MW;
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PROSITE; PS00633; BROMODOMAIN.2; 1.
PROSITE; PS50014; BROMODOMAIN.2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       trithorax."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and expression pattern strong homology to ALL-1 involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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to Drosophila
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seq_documentation_block:
ID 014686
AC 014686;
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JAN-1998 (TrEMBLrel. 05
DT 01-JUN-2001 (TrEMBLrel. 17
DE ALR.

OS Homo sapiens (Human).
C Eukaryota; Metazoa; Chorda
OC Mammalia; Eutheria; Primat
OX NCBL_TAXID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97388474; PubMed-9
RA PATASAD R., Zhadanov A.B.,
RY STUCEUre and expression |
RT strong homology to ALL-1 i
RT crithorax.";
STUCEUre and expression |
RT structure and expression |
RT trithorax.";
RT [15:549-560(1997).
RI Oncogene 15:549-560(1997).
RI InterPro; IPR001822; Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded Recombourded
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US-09-684-016-48411 x 014687
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    Quality:
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MEDLINE-97388474; PubMed-9247308;

Prasad R., Zhadanov A.B., Sedkov Y., Bullrich F., Druck T.,

Rallapalli R., Yano T., Alder H., Croce C.M., Huebner K., Mazo A.,

Canaani E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
SMART;
SMART;
SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF010403; AAC51734.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 15:549-560(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure and expression pattern strong homology to ALL-1 involved
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SM00249;
SM00508;
SM00317;
NCE 4957
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IPR001214; SET.
IPR001822; Recombinase.
IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                IPR001965; PHD. IPR002965; P_rich_extensi.
                                                                                                                                                                                                                                                                                                                                                           IPR003616; PostSET
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; PHD; 4.
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; SET; 1.
; AA; 531848 !
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Primates;
       1.
564181 MW;
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Last annotation updat
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         26B7C74CAD417E44 CRC64;
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in acute leukemia
                                                                                                                                                                                                                     UNKNOWN_1.
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seq_documentation_block:
ID 022662:
PRELIMINA
AC 022662:
PT 01-NOV-1996 (TrEMBLre
DT 01-NOV-1996 (TREMBLRE
DT 01-JUN-2001 (TREMBLRE
DT 01-JUN-2001 (TREMBLRE
DT 01-JUN-2001 (TREMBLRE
DT 01-JUN-2001 (TREMBLRE
DT 01-JUN-2001 (TREMBLRE
DE 722C1.1
OS Caenorhabditis elegar
OC EMARYOCE: Metazoa; h
OC Rhabditidae; Peloderi
OX NCBI_TAXLD=6239;
RN [1]
RN [2]
RN [2]
RN SEQUENCE FROM N.A.
RA MCMULTRAY A.;
RL SUDMITTED (JUN-1996)
RN SEQUENCE FROM N.A.
RA MCMULTRAY A.;
RA MEDLINE=94150718; Pul
RA BONFIELD J., Burton,
RA Craxton M., Dear S.,
RA Gardner A., Green P.
RA Jones M., Kershaw J.
RA Jones M., Kershaw J.
RA Jones M., Kershaw J.
RA Jones M., Kershaw J.
RA Jones M., Smith A.
RA Thierry-Mieg J., Thon
RA Watson A., Weinstock
RT 12.2 Mb of contiguou
RT elegans.;
RA InterPro; IPR003126;
DR Pfam; PR02207; zf-UB
DR SEQUENCE 416 AA;
                                                                                                                                          alignment_block:
US-09-684-016-48411 x Q22662
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US-09-684-016-48411 x O14686
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    Quality:
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                                                                                                Align seg 1/1 to:
                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                         EMBL; 27550; CAA99920.1; -.
InterPro; IPR003126; ZnF_UBR1.
Pfam; PF02207; Zf-UBR1; 1.
SMART; SM00396; ZnF_UBR1; 1.
SEQUENCE 416 AA; 47619 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Lister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1135 CyshisalaProTyrValGluGluAspLeuLeuIleGlnCysArgHisCy 1251
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 CACTGACTGG 73
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LysPheCysThrCysAspValPheTyrProAspGluAspGlyGlyLysGl 213
                                              AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGAC.....CT
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                                                                                                                                                                                                                                                                Quality:
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                                                                                                Q22662
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3.719
59.259
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                                                                                                                                                                     Percent Identity: 37.037
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Gaps: 0
Identity: 45.000
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seq_documentation_block:
ID Q970Al;
AC Q970Al;
AC Q970Al;
DT Q1-MAY 2000 (TrEMBLrel. 13
DT Q1-MAY 2001 (TrEMBLrel. 13
DT Q1-MAY 2001 (TrEMBLrel. 13
DT Q1-MAY 2001 (TrEMBLrel. 13
DT Q1-JUN 2001 (TrEMBLrel. 13
DT Q1-JUN 2001 (TrEMBLrel. 17
DE HYPOTHETICAL 49.7 KDA PROT
GN T32Al6.30 OR A74233660.
OS Arabidopsis thaliana (Mous
OC Eurosids II; Brassicales;
OX Spermatophyta; Magnoliophy
OC eurosids II; Brassicales;
OX (EBL_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Zimmermann W., G
RA Mewes H.W., Mayer K.F.X.,
RL Submitted (MAY-1999) to th
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing
RL Submitted (MAY-1999) to th
RN [3]
RP SEQUENCE FROM N.A.
RA Zimmermann W., Grueneisen
RA Zimmermann W., Grueneisen
RA Zimmermann W., Grueneisen
RA Zimmermann W., Grueneisen
RA Smith A., Mewes H.W., Lemc
RL Submitted (MAR-2000) to th
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing
RL Submitted (MAR-2000) to th
RN [4]
DR SEQUENCE FROM S.A.
RA EU Arabidopsis CAB81304.1
DR InterPro; IPR001955; PHD.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00628; PHD; 1.
DR Pfam; PF00628; FTUBR1; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR SMART; SM00249; AF044
seq_documentation_block:
ID Q9VRV6 PRELIMI
AC Q9VRV6;
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US-09-684-016-48411 x Q9T0A1
                                                                                                          seq_name: sp_invertebrate:Q9VRV6
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                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q9TOA1 from: 1 to: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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Q9TOA1;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 49.7 KDA PROTEIN.
T32A16.30 OR AT4623860.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                              128 TyrCysThrCysAspArgProTyr...ProAspProAsnValGluGluGl 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00249; PHD; 1.
SMART; SM00396; ZnF_UBR1; 1.
Hypothetical protein.
SEQUENCE 443 AA; 49704 MW
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InterPro; IPR003126; ZnF_UBR1.
Pfam; PF00628; PHD; 1.
Pfam; PF02207; zf-UBR1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL078468; CAB43886.1; -.
EMBL; AL161560; CAB81304.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P., Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft I., Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    143 nValGluMetIleGlnCysCysLeuCysGluAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                           Quality:
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                            PRELIMINARY;
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Percent Identity:
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alignment_block:
US-09-684-016-48411/rev
                                                                                                                   alignment_scores:
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RS Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Horly J.H., Agbayani A. An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
RA Gerson K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerson K.K., Doup L.E., Downes M., Duyan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferriera S., Pleiscohmann W.,
Rosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lang Y., Lii X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Jan K.,
RA Mount S.M., Woylan K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Woylan K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Woylan K., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Woylan K., Sunders R.D.C., Scheeler F., Shan H.,
RA Shee B.C., Sidan T., Shang M., Shoeler F., Shan H.,
RA Shee B.C., Sidan
                                                            Percent Similarity:
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01-MAY-2000
01-JUN-2001
CG7386 PROTE
CG7386.
                                                                                                                                                                         PROSITE; PS00028; ZINC_FINGER_C2H2_1; 10.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
DNA-binding; Metal-binding; Zinc-finger.
SEQUENCE 662 AA; 76582 Mm. Central.
                                                                                                                                                                                                                                                                            InterPro; IPR000822; 2nf-C2H2.
InterPro; IPR000130; 2n_MTpeptdse.
Pfam; PF00096; zf-C2H2; 12.
SMART; SM00355; Znf-C2H2; 12.
                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0035691; CG7386
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                           Quality:
Ratio:
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                                                          Percent Identity:
                                                                                                                                                                                258BE838CF67A8E9 CRC64;
                                                        33
1
36.364
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DT DT DT DT DT
                                                                     seq_documentation_block:
ID Q9BQW0 PRELIMINARY;
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Quality:
                                                                                                             seq_name:
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                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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 01-JUN-2001
01-JUN-2001
DJ885L7.9.3
                                                                                                                                         1473 sAsnCysLeuGluTrp
                                                                                                                                                                                                  1457 CysLeuCysArgGlnProPheAlaIleSerAspGlyThrValGlnCysHi
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Q9UT79;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN, PHD FINGER.
SPAC343.11C.
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                                         Q9BQW0;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS01180; EGF_2; UNKNOWN_1.
SMART; SM00249; PHD; 3.
SMART; SM00249; PHD; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003347; JmjC.
InterPro; IPR003349; JmjN.
Pfam; PF00628; PHD; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomycetales;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 LeuValPheSerArgLeuArgLeu...LeuThrIleHisLeuLysLysVa 279
                                                                                                                                                                       58
                                                                                                                                                                      GGGCTGCACTGACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTGTGTGGAATAAATTGAAGATAAGTATCACCTTACATGTGAAACTTAC 73
                                                                                                             sp_human:Q9BQW0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02373;
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(TYEMBLrel. 17, Created)
(TYEMBLrel. 17, Last sequence update)
(TYEMBLrel. 17, Last annotation updat
(DEATH ASSOCIATED TRANSCRIPTION FACTO
                                                                                                                                                                                                                                                          Q9UT79
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AA;
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update)
FACTOR 1
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 (CONTAINS
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Quality:
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Submitted (NOV-2000) to the EMBL/GenBank/DDBJ
EMBL; BC000770; AAH00770.1; -.
Hypothetical protein.
SEQUENCE 544 AA; 59487 MW; 193341A77ED5FAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
17, University (Trembler)
17, Last annotation update)
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TISSUE=KIDNEY ADENOCARCINOMA;
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Mammalia; Eutheria;
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sAspArgCysGluGluTrp 291
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                                                                                                                 CGAGGGCTGCACTGACTGG
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    Quality:
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A ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

AN Ishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

AN Ishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

AN Ishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

AN Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

AN Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

AN Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

AN Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,

AN Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.";

AN Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.";

Submitted (FEBP-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO02127; BAA92094.1; -.

InterPro; IPR001965; PHD.

BR FAMRT; SM00249; PHD; 1.

SEQUENCE 562 AA; 61425 MW; 3BA79F8DEF9D3D9C CRC64;
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TISSUE-COLON ADENOCARCINOMA;
Strausberg R.;
Submitted (MAR-2001) to the EI
EMBL; BC004237; AAH04237.1; -
Hypothetical protein.
SEQUENCE 562 AA; 61353 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    documentation_block:
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                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 61.4 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat;
Eukaryota; Metazoa; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NUMB PRELIMINARY; PRT; 562 AA.
Q9NUMB;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CDNA FLJ11265 FIS, CLONE PLACE1009158.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9BTC0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BTC0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 sAspArgCysGluGluTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy 285
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3.531
69.565
61353 MW;
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                                                                                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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       91A714668F9C5C12
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39.130
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                                                                                                           databases
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seq_name:
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US-09-684-016-48411 x Q9WV00
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Quality:
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US-09-684-016-48411 x Q9BTC0
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                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
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Q9WV00 PRELIMINARY;
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Q9WV00;
Ol-NOV-1999 (TrEMBLrel. 12, Created)
Ol-NOV-1999 (TrEMBLrel. 12, Last sequence up
Ol-JUN-2001 (TrEMBLrel. 17, Last annotation
DEATH INDUCER-OBLITERATOR-1 (FRAGMENT).
DIDO1 OR DIO-1.
DIDO1 OR DIO-1.
                                                                                                                                                                                                                                                                                                                                                    misexpression disrupts limb development,";
proc. Natl. Acad. Sci. U.S.A. 96:7992-7997(1999).
EMBL; AJ238332; CABA8401.1; -
MGD; MGI:1344352; Dido1.
InterPro; IPR001965; PHD.
Pfam; PF00628; PHD; 1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
SNART; SM00249; PHD; 1.
SNART; SM00249; PHD; 1.
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Garcia-Domingo D., Leonardo E., Grandien A., Martinez P., Izpisua-Belmonte J.C., Martinez-A C.;

"DIO-1 is a gene involved in onset of apoptosis in vitro,"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                              282 sAspArgCysGluGluTrp 288
                                                                                                                                     267 TyrCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                   sp_vertebrate:Q9W664
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              PRELIMINARY;
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3.531
69.565
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              PRT;
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Identity:
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              641
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39.130
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seq_documentation_block:
ID 015043;
AC 015043;
AC 01-JAN-1998 (TrEMBLrel 05
DT 01-JAN-1998 (TrEMBLrel 05
DT 01-JUN-2001 (TrEMBLrel 17
DE KIAA0333 (FRAGMENT).
GN KIAA0333 (FRAGMENT).
GE WATAA0333 (FRAGMENT).
CE EUKARYOTA; Metazoa; Chorda OC Mammalia; Butheria; Primat OX NCBI_TAXID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=97349984; PubMed=9
RA Magase T., Ishikawa K., Ne
RA Tanaka A., Kotani H., Nomu
RT "prediction of the coding
RT The complete sequences of
RT code for large proteins ir
COMBL; AB002331; BAA20791.]
DR Interpro; IPR001052; Rubré
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InterPro; IPRO0160; SAM.
Pfam; PF00870; P53; 1.
PRINTS; PR00386; P53SUPPRESSR.
PRINTS; PR002681; P53; 1.
SMART; SM00454; SAM; 1.
SEQUENCE 641 AA; 71090 MW;
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01-NOV-1999
01-JUN-2001
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                                        code for large proteins in vitro. DNA Res. 4:141-150(1997).
                                                                      Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                      KIAAU333.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              520 ........GlyLeuGlnSerValTyrHisLeuGln 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 HisCysThrProProProProTyrAsnProAspProSerLeuValSerPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barbus barbus (Barbel).
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprininae; B
                                                                                                                                                  MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503 eLeuThrSerLeuGlyCysGlnAsnCysIleAspTyrPheThrSerGln.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=40830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_human:015043
                        AB002331; BAA20791.1; -
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(TrembLrel. 12, Last seq
(TrembLrel. 17, Last ann
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2.260
55.556
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Last annotation updat
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                             " cDNA clones
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Euteleostei; Ostariophysi
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seq_documentation_block:
ID Q944G6
AC Q944G6
DT Q1-MAR-2001 (TrEMBLIE
DT Q1-MAR-2001 (TrEMBLIE
DT Q1-MAR-2001 (TREMBLIE
DT Q1-JUN-2001 (CONTAINS K
GN DJ885L7-9.1 (CONTAINS K
GN DJ885L7-9.1 (CONTAINS K
GN HOMO Sapiens (Human).
OC EUKARYOTA; Metazoa; C
OC Mammalila; EUTheria; F
N (L1] TAXID=9606;
RN [1] TAXID=9606;
RN [1] TAXID=9606;
RN SEQUENCE FROM N.A.
RA Smith M.;
SUDMITTED (COT-2000)
BR SEQUENCE JER001965;
DR INTERPO; IPR001209;
DR INTERPO; IPR001209;
DR INTERPO; IPR003618;
DR PART; SM00528; PHD; 1
DR SMART; SM00510; TF82A
DR PROSITE; PS00527; RII
FT NON_TER
SQ SEQUENCE 1042 AA;
                                                                                                                                                                     alignment_scores:
    Quality:
    Ratio:
                                                                                          alignment_block:
US-09-684-016-48411 x Q9H4G6
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Quality:
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                                                        Align seg 1/1 to: Q9H4G6 from: 1
                                                                                                                                                     Percent Similarity:
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Percent Similarity:
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ885L7.9.1 (NOVEL PROTEIN SIMILAR TO MOUSE DEATH INDUCER OBLITERATOR
1 (DIO-1) (CONTAINS KIAA0333) (ISOFORM 1)) (FRAGMENT).
DJ885L7.9.
                                                                                                                                                                                                                                                                                                     SMART; SM00249; PHD; 1.
SMART; SM00510; TFS2M; 1.
PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001965; PHD.
InterPro; IPR001209; Ribosomal_S14.
InterPro; IPR003618; TFS2_cent.
Pfam; PF00628; PHD; 1.
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PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
SMART; SM00249; PHD; 1.
SMART; SM00510; TFS2M; 1.
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InterPro; IPR001965; PHD.
InterPro; IPR003618; TFS2_cent.
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                TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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    Quality:
    Ratio:
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                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q9YEG2
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-684-016-48411/rev x Q9YEG2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.
A Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kost
A Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
A Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
Tranarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
R EMBL; AP000060; BAA79564-1; --
R InterPro; IPR000566; Lipocin_cytPABP.
RPOSITE; PS00213; LIPOCALIN; UNKNOWN_1.
W Hypothetical protein; Complete proteome.
O SEQUENCE 544 AA; 55839 MW; 14028D4D558A7891 CRC64;
                                                                                                                                                                        documentation_block:
Q9RLR4 PRELIMINARY;
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         Legionella pneumophila.
Bacteria; Proteobacteria;
Legionellaceae; Legionella
RCBI_TaxID=446;
                                                                                                        Q9RLR4;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                    195 rCysSerProArgIleAlaAlaLeuGly 204
                                                                                                                                                                                                                                                                                                                 179 TrpGluProIleAspAlaValPheLysValGluIleGluLeuAspArgSe 195
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 55.8 KDA PROTEIN APE0614.
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                                                                                                                                                                                                                                                                                  66 GTGCAGCCCTCGCATTGCGCCATTAGGT
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                             Legionella
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Last sequence update)
Last annotation updat
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                                              subdivision; Legionellaceae
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ai A., Kosugi
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STRAIN-PHILADELPHIA-1;

X MEDLINE-20032053; PubMed-10564519;

X Segal G., Russo J.J., Shuman H.A.;

"Relationships between a new type-IV secretion sys virulence system of Legionella pneumophila.";

RL Mol. Microbiol. 34:799-809(1999).

DR EMBL; Y19029; CAB60060.1; -

EMBL; Y19029; CAB60060.1; -

EMBL; Y19029; CAB60060.1; -

RE MOL. Microbiol. 363 AA; 39117 MW; F23E77A30A279BC7 (
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                 Pfam; PF01426; BAH; 1.
Pfam; PF00439; bromodomain; 1.
Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
SMART; SM00384; AT_hook; 3.
SMART; SM00249; BAH; 1.
SMART; SM00297; BROMO; 1.
SMART; SM00297; BROMO; 1.
SMART; SM00299; PHD; 1.
SMART; SM00317; SET; 1.
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Q9NR48 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDILINE-20319018; PubMed=10860993;

MEDILINE-20319018 J., Tada S., Rozovskaia T.,

Nakamura T., Blechman J., Tada S., Rozovskaia T.,

Bullrich F., Mazo A., Croce C.M., Geiger B., Cana

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homologue of the Drosophila ash1 gene, localizes

cell-cell tight junctions.",

Proc. Natl. Acad. Sci. U.S.A. 97:7284-7289(2000).

EMBL; AF257305; AAF68983.1; -
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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01-OCT-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
  PROSITE;
                                                                                                                                                                                                                                                                                              InterPro; IPR000637; AT_hook.
InterPro; IPR001025; BAH.
InterPro; IPR0011487; Bromodomain.
InterPro; IPR001965; PHD.
InterPro; IPR003616; PostSET.
InterPro; IPR001214; SET.
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seq_documentation_block:
ID 09H0S7 PRELIMINA
AC 09H0S7;
DT 01-MAR-2001 (TrEMBLre
DT 01-MAR-2001 (TrEMBLre
DT 01-JUN-2001 
ON PROTESTE (Human)
OC EUKARYOTA; Metazoa;
OC Mammalia; Eutheria;
OC MAMMalia; Eutheria;
OC MAMMalia; Eutheria;
OC MAMMalia;
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US-09-684-016-48411 x Q9H0S7
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SQ
seq_name: sp_invertebrate:Q9XWD7
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                                                                                                                           111 ATTCCACACAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 180 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-BRAIN,
Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J.,
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL136660; CAB66595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09H0S7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50280; SI SEQUENCE 2969 AA;
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PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
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                                                                    93 yrSerThrLys
                                                                                                                                                                                         76 nIlePheAspTrpAsnValLysGlnLeuPheLeuTyrLeuSerAlaGluT
                                                                                                                                                                                                                                                       61 CTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAATTT 110
                                                                                                                                                                                                                                                                                                                     60 ArgSerAspLeuGlyPheIleThrSerAspIleThrAlaAspLeuGluAs
                                                                                                                                                                                                                                                                                                                                                                                   11 AAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGAGGG
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A; 332765 MW;
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US-09-684-016-48411/rev x Q9XWD7
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01-JUN-2001 (Tr
GB(AAC80581.1.
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                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL032657; CAA21738.1; -. InterPro; IPR001594; Znf-DHHC. Pfam; PF01529; Zf-DHHC; 1. ProDom; PD003041; Znf-DHHC; 1. SEQUENCE 368 AA; 41180 MW;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
747H9C.2 PROTEIN.
STRAIN-COLUMBIA;
                          SEQUENCE FROM N.A.
                                                                                 NCBI_TaxID=3702;
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Ratio:
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45.833
                                                                                                                                                             Tracheophyta;
                                                                                                                                   Rosidae;
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US-09-684-016-48411 x Q9FNI5
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Percent Similarity:
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Q9U263;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-JUN-2001 (TrEMBLrel. 17, L
Y51H4A.12 PROTEIN.
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InterPro; IPR001965; PHD.
Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 3.
PROSITE; PS00018; EF_HAND; UNK
SEQUENCE 1516 AA; 170012 MW
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                                                                                                                                                                                             Pfam; PF00628; PHD; 1.
Pfam; PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
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DNA Res. 4:291-300(1997).
                                                                                                                        SMART; SM00249; PHD;
SMART; SM00317; SET;
SEQUENCE 1645 AA;
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InterPro; IPR001214; SET.
InterPro; IPR001965; PHD.
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                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                    Genome sequence of the nematode C.elegans: A platform
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a; 170012 MW; FFAAA8593BA93CEA CRC64;
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US-09-684-016-48411 x O44498

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Pfam; PF00856; SET; 1.
PROSITE; PS50280; SET; 1.
SMART; SM00249; PHD; 1.
SMART; SM00317; SET; 1.
SEQUENCE 1655 AA; 18258
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O44498 PRELIMINARY;
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Submitted (DEC-1997) to the
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STRAIN=BRISTOL N2;
Miller N., Stellyes L.,
Submitted (DEC-1997) to
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Eukaryota; Metazoa; Ner
Rhabditidae; Peloderina
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InterPro; IPR001214; SET.
InterPro; IPR001965; PHD.
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                                                                                       182580 MW;
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to the EMBL/GenBank/DDBJ databases
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                                                         Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                          0AB49D12CB1C0686 CRC64;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., How, Hoskins R.A., Galle R.F.,
RA Barndon R.C., Rogers Y.H.C., Blazej R.G., Chang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Barlew R.C., Rogers Y.H.C., Blazej R.G., Chang O., Chen L.X.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Byanaktaroglu L., Beasley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Bodson K., Doup L.E., Downes M., Duyan Rocha S., Dunkov B.C., Dunn P.,
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RA Dodson K., Doup L.E., Downes M., Duyan Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N., Kalush F., Karpen G. H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N., Wattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D. Lai Z.,
Lai Z., Liang Y., Lia Z.,
Lai Z., Liang Y., Lia Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Rount S.M., Mood R., Stonders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stden Kimmel B.A., Walson K.A., Mixon K., Mixon R., Walson N., Strond R., Sun B.,
RA Sulfaks R., Tector C., Tunner R., Venter E., Wang A.H., Wang X.,
RA Shue B.C., Stden R., Shang M., Venter J.C.,
RA Gibbs R.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: sp_invertebrate:Q9VR08
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Q9VR08;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-JUN-2001 (TrEMBLrel.
CG15637 PROTEIN.
                                        EMBL; AE003576; AAF51000.1;
HSSP; P35555; 1EMN.
                      FlyBase; FBgn0000488; dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836 uGlyCysLysThrTrp 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      821 CysHisCysGlyMetAspHisGlyAspGlyAspThrIle...GluCysGl 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGCTGCACTGACTGG
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IPR000152; Asx_hydroxyl
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Last annotation update)
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to:
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seq_documentation_block:
ID Q9Y7S1;
AC Q9Y7S1;
DT 01-MAY-2000 (TrEMBLEG
DT 01-MAY-2000 (TREMBLEG
DT 01-MAY-2000 (TREMBLEG
DT 01-MAY-2000 (TREMBLEG
DT 01-MAY-2000 (TREMBLEG
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DT 01-MAY-2000 (TREMBLEG
DE CG5065 PROTEIN.
GN CG5065 PROTEIN.
GN CG5065 PROTEIN.
GN CG5065 PROTEIN.
OC EMPAGROCIA; Neoptera;
OC EMPAGROCIA; Neoptera;
OC EMPAGROCIA; Neoptera;
OC EMPAGROCIA; Neoptera;
OC EMPAGROCIA; Neoptera;
RN [1]
RN [1]
RN GEDLINE-20196006; Put
RA Adams M.D. Celniker
RA Adams M.D. Celniker
RA Adams M.D. Celniker
RA Adams M.D. Celniker
RA Adams M.D. Celniker
RA BEGOTGE R.O., Wortman
RA BEGOTGE R.O., Wortman
RA BEGOTGE R.O., Wortman
RA BEGOTGE R.O., BOSQUA
RA BEGON K.H., DOYLE C., I
RA BEGON K.H., DOYLE C., I
RA BEGON K.G., BUSAMD D
RA CHERTY J.M., CAWLEY;
RA DOGSON K., DOUD L.E.,
RA DURDIN K.J., Evangel:
RA DURDIN K.J., Evangel:
RA DURDIN K.J., Evangel:
RA Glodek A., Gong F., (
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Quality:
Ratio:
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US-09-684-016-48411 x Q9VR08
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An Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An Annatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
An George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
An Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An Haril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
An Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottlier P.,
An Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
An Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
An Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
An Dodson K.J., Evangelista C.C., Ferriac S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
An Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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ProDom; PF0003573; ET; 1.
SMART; SM00179; EGF_CA; 16.
SMART; SM000101; EGF_11ke; 35.
SMART; SM0020274; FOLN; 5.
SMART; SM00289; WR1; 2.
PROSITE; PS001010; ASX_HYDROXYL; 18.
PROSITE; PS00110; ASX_HYDROXYL; 18.
PROSITE; PS01186; EGF_1; 1.
PROSITE; PS01187; EGF_CA; 17.
Calcium-binding; EGF-11ke domain; G1
SEQUENCE 3680 AA; 388637 MW; E5E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropóda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20196006; PubMed=10731132; Adams M.D., Celniker S.E., Holt R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTGTAAATGTGAG....ATGCCTTACAACCCTGATGACCTAATGGC
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IPR000561;
IPR001881;
IPR002603;
IPR003645;
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(TrEMBLrel. 13,
(TrEMBLrel. 13,
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3.633
62.500
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E5E972E1A3479EFF CRC64;
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alignment_block:
US-09-684-016-48411 x Q9V7S1
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    Quality:
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McFkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A., Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A., Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Meinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zhens R.A., Myers E. W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
EMBL; AED03806; AAF57974.1: -
DR EMBL; AED03806; AAF57974.1: -
DR SEQUENCE 625 AA; 69682 MW; 8C12CD780F96D5E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q9V7S1 from: 1 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       024459
024459;
-!- SIMILARITY: CONTAINS 2
EMBL; L35153; AAA64457.1;
FlyBase; FBgn0003044; Pcl.
InterPro; IPR001965; PHD.
InterPro; IPR002999; Tudor
                                                                                                                       MEDLINE=95044940; Pubmeu-, Saint R.;
Lonie A., D'andrea R., Paro R., Saint R.;
"Molecular characterisation of the Polycomblike
"Molecular characterisating negative regulator
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                      Development 120:2629-2636(1994).
                                                                                                          melanogaster, a trans-acting expression.";
                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-ISOGENIC CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                           POLYCOMBLIKE NUCLEAR PROTEIN. PCL.
                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 TyrCysAsnCysAspArgThrAspValSerGluValIleTyrAlaProPr 286
                                                                                                                                                                                                                                                               NCBI_TaxID=7227;
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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3.857
56.000
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                                                                        PHD-FINGER DOMAINS
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36.000
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of ho
                                                                                                                               homeotic
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Quality:
Ratio:
RX MEDLINE-20196006; PubMed-10731132;

RX MEDLINE-20196006; PubMed-10731132;

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., It P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Buril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: sp_invertebrate:Q9V8C2
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DOMAIN 242 256
DOMAIN 274 277
DOMAIN 327 341
DOMAIN 408 411
DOMAIN 424 472
DOMAIN 512 566
DOMAIN 843 846
DOMAIN 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9V8C2; PRELIMINARY;
Q9V8C2; O1-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
PCL PROTEIN.
PCL OR CG5109.
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O9V8C2 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00628; PHD; 2.
SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR;
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4.500
52.174
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Gaps: 0
Percent Identity: 43.478
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Last annotation update)
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POLY-PRO.
POLY-GLY.
PHD-FINGER.
PHD-FINGER.
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seq_documentation_block:
ID Q9FK65
AC Q9FK65;
AC Q9FK65;
AC Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-MAR-2001 (TrEMBLrel. 16
DT Q1-JUN-2001 (TrEMBLrel. 17
DE RECEPTOR-LIKE PROTEIN KINA
OS Arabidopsis thaliana (Mous
OC Eukaryota; Viridiplantae;
OC Spermatophyta; Magnoliophy
OC eurosids II, Brassicales;
OX NCBL_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-COLUMBIA;
RX MEDLINE=98403884; PubMed=9
RA Tabata S.;
RT "Structural analysis of Ar
RAT Tabata S.;
RT "Structural analysis of Ar
RAT Tabata S.;
RT "Structural analysis of Ar
RAT Sequence features of the r
RT Sequence features of the r
Physically assigned P1 and
RL DNA Res. 5:203-216(1998).
DR EMBL; AB012245; BAB09221.1
DR InterPro; IPR000719; Buk_p
DR InterPro; IPR000719; ENL_D
DR InterPro; IPR001611; LRR.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR001611; LRR.
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                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR-LIKE PROTEIN KINASE.
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                              physically assigned P1 and TAC DNA Res. 5:203-216(1998). EMBL; AB012245; BAB09221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      529
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SMART; SM00249; PHD; 2.
SMART; SM00333; TUDOR; 1.
SEQUENCE 1042 AA; 114506 MW;
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InterPro; IPR001965; PHD.
InterPro; IPR002999; Tudor
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                                                                                                                                                                   Tabata 5.;
"Structural analysis of Arabidopsis thaliana of the regions of 1,367,185
                                                                                                                                                                                                                                                                  MEDLINE=98403884; PubMed=9734815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55 CGAGGGCTGCACTGACTGG
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                                                                         IPR000719; Euk_pkinase.
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4.500
52.174
LRR_out.
Ser_thr_kin_actsite
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                                                                                                                                                   clones.";
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Gaps:
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43.478
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                                                                                                                                                                          covered
                                                                                                                                                                                                                                                                                                                                                                                                       eudicots; Rosidae;
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Moshrefi A.,
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Tyr_kin.

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seq_documentation_block:
ID 099G78;
AC 099G78;
DT 01-MAY-2000 (TrEMBLre
DT 01-MAY-2001 (TrEMBLre
DT 01-JUN-2001 (TrEMBLre
DT 01-JUN-2001 (TrEMBLre
DT 01-JUN-2001 (TrEMBLre
DT 01-JUN-2001 (TrEMBLre
DE CG6525 PROTEIN.
GN CG6525.
OS Drosophila melanogast
OC Ethydroidea; Drosophi
OX Perygota: Neoptera;
OC Ephydroidea; Drosophi
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=70196006; Pul
RA Adams M.D., Celniker
RA Adams M.D., Celniker
RA George R.A., Lewis S
RA Sutton G.G., Wortman
RA Berson K.D., Poyle C., I
RA Barandon R.C., Rogers
RA Barlew R.M., Basu A.
RA Beeson K.H., Doyle C., I
RA Ballew R.M., Basu A.
RA Beeson K.J., Busam D
RA Cherry J.M., Cawley
RA George R.A. Doup L.E.
RA Durbin K.J., Cawley
RA Glodek A., Gong F.,
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US-09-684-016-48411/rev x Q9FK65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Bartil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktarroglu L., Beasley E.M.,
RA Bellew R.M., Basu A., Banendale J., Bayraktarroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: sp_invertebrate:Q9VG78
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PRINTS; PRO0109; TYRKINASE.
SMART; SM00370; LRR; 4.
SMART; SM00221; STYKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYFKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 570 AA; 63537 MW; 972414BDE3A8DBC0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spValLysAlaAlaAsnIle 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lTyrLeuHisGluGlnCysAsnProLysIleIle......HisArgA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TrpAsnArg...ArgIleSerIleAlaLeuGlyAlaAlaArgGlyLeuVa
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Gaps: 3
Percent Identity: 40.000
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alignment_scores:
    Quality:
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kunip D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lilang Y., Lin X.,
RA Lasko P., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcikulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittana G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R., F., Zaveri J.S., Zhan M., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.,
RI Science 287:2185-2195(2000).
RDR HISTORIAN SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL SCHOOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
                                                                                                                                                                                                                   Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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SMART; SM00510; TFS2M; 1.
SEQUENCE 2016 AA; 221998 MW;
                                                                                  Submitted
                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                Q98VX5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            927 sAspLeuCysGluAspTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912 TrpCysIleCysArgGlnProHisAsn...AsnArgPheMetIleCysCy
                                                             Mandal D., Chakrabarti S.;
"Divergent HIV-1 C subtypes
Submitted (MAR-2001) to the
EMBL; AJ311641; CAC34551.1;
                                                                                                                                                                                                                                                                                                               ENVELOPE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                      Q98VX5;
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InterPro; IPR001965; PHD.
InterPro; IPR003618; TFS2_cent.
InterPro; IPR003628; PHD; 1.
SEQUENCE
                     NON_TER
                                          NON_TER
                                                                                                                                                        STRAIN-IND.CAL1058;
                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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AA;
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22154 MW;
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Percent Identity:
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Last annotation update)
                                                                                    isolated from Calcutta, India.";
EMBL/GenBank/DDBJ databases.
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51583AFEOBF1EDC1 CRC64;
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39.130
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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123
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Copyright (c) 1993 - 2000 Comp
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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682	655	635	586	514	574	543	497	540	764	765	530	ength
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AW584948	AW584724	AW584723	BE997991	AW586761	BE124753	AW616232	BG551208	AW432561	AW349333	BE659470	AW761136	ID
AW584948 N211110e		w		AW586761 EST318384					AW349333 GM210007A	BE659470 GM700009B	AW761136 s163f12.y	Description

Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or

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BE519330	BE214475	BE346433	AW448025 ·	BG606610	AU084649	AI026312	AI443020	.BG605406	BF650924	AW459464	BG300821	AU101324	BF474495	BF275530	BE639441	AI726030	AI759012	BE123398	AI731699	BG320550	BG643885	BG605300	AI987319 ·	BE418763	BE039612	BE037301	BG048538	BG887479	BI208519	AW035325	AI486129	BG551127
945	BE214475 HV_CEb000	sp2	BRY	HE	AU0	L0-529	sa30h0	WHE232	BF650924 NF098E01E	sh41e1	BG300821 HVSMEb001	AU101324 AU101324	BF474495 WHE0844_G	BF275530 GAEb002	BE639441 946033B11	AI726030 BNLGH1139	AI759012 605085F11	BE123398 946001F06	AI731699 BNLGHi105	BG320550 Zm03_10h1	BG643885 EST512079	BG605300 WHE2331_B	AI987319 660003H05	BE418763 SCL074.H0	BE039612 OC01G11 O	BE037301 MP19C11 M	OV1_14_H	EST51333	BI208519 EST526559	EST28068	EST24445	BG551127 sad33f01.

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ALIGNMENTS

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JOURNAL COMMENT REFERENCE AUTHORS VERSION KEYWORDS SOURCE RESULT AW761136 LOCUS DEFINITION ACCESSION TITLE ORGANISM Shoemaker,R., Keim,P., Vookin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA AW761136 530 bp mRNA EST 21-NOV-2000 s163f12.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-6024 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN Glycine max Glycine Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae AW761136 AW761136.1 GI:7693038 , mRNA sequence. (bases 1 to 530) Phaseoleae;

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RESULT 2
BE659470/c
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Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                             BE659470 765 bp mRNA EST 24-MAY-2001 GM700009B10H8 Gm-r1070 Glycine max cDNA clone Gm-r1070-3447 3',
                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  first-strand synthesis primer was used. An anchor nucleotide (V=A, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAGAGAGAGTAGTTTGGAG(T)]8] to anchor the primer at the 5' end of the poly(A) tract. After second- strand synthesis, the cDNA ends were filled in with cloned pfu DNA, ligated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript(tm) II XR predigested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n-30). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthexix Kit (catalog number 200401) was used to synthesize the cDNA. First stranded synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for CDNA synthesis. Stratagene's CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xhoi; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="cotyledons of 3- and 7-day-old Williams
seedlings"
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/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1027-6024"
/clone_lib="Gm-c1027"
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                                                                                                                           482 CACTGACTGGT 472
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                                                                                                                                                                                                                                                      4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg 63
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Other_ESTs: AW432561 corresponding to Gm-c1015-5652 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program
Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vodkin,L., Keim,P., Shoemaker,R., Retzel,E., Khanna,A., Erpelding,J., Raph,C., Shoop,E., Pardinas,J., Liu,L. and A Functional Genomics Program for Soybean (NSF 9872565)
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ystems.com web site:www.genomesystems.com seg primer: 5'-TTTTTTTTTTTTTTTTTT(A/C/G)-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134. For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact:clones@genomesystems.com or info@genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwin R. Madigan Building,
Tel: (217) 244-6147
Fax: (217) 333-4582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5'. EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The deta information on the source library for each clone can be obtained by referring to the Genome Systems clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a representative of each contig, which were reracked to form library Gm-r1070. The cDNA clones of the reracked Gm-r1070 library were then sequenced at the 3' end. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keck Center for Comparative and Functional Genomics, University of Illinois,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Center for Computation
Genomics and Bioinformatics, University of Minnesota,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="The library Gm-r1070 is a sequence-driven, reracked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the original cDNA library that is also 'OTHER EST'."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomesystems.com,
Keck Center for Comparative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html
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95.8%;
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764 bp
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                                                                                                                                                                                                                                           Local
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GTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGTCCAATGTGAGGGCTG 507
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Other_ESTs: AI461129
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A Functional Genomics Program
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Seq primer: 5'.TTTTTTTTTTTTTTTTT(A/C/G)-3'.
Location/Qualifiers
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Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA
Tel: (217) 244-5147
Fax: (217) 333-4582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the laboratory of Linesota, Centers, University of Minnesota, the http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html http://www.cbc.umn.edu/ResearchPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     day old "Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA Synthesis Kit (catalog #200401) was used to synthesize the cDNA. The Gm-c1004 library was constructed by Dr. Paul Keim & Virginia H. Coryell, Department of Biology, Box5640, Northern Arizona University, Flagstaff, Az 86011 email: paul keim@nau.edu. virginia.coryell@nau.edu. The contig analysis to select unique genes was performed by the laboratory of Ernest Retzel, Computational Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.life.uiuc.edu/biotech/keck.html."
161 c 151 g 193 t 20 others
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/clone="Gm-r1021-2316"
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95.8%;
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Insert Length: 1008 Std Error: 0.00
Seq primer: -40RP from Gibco
High quality sequence stop: 380.
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from mature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR cDNA library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally
                                                                                                                                                                                                                                                                cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into XL10-Gold host cells. This library was
                                                                                                                                                                                                            Erpelding."
                                                                                                                                                                                                                                        constructed by Dr. Randy Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="GENOME SYSTEMS CLONE ID: Gm-c1015-5652"
/clone_lib="Gm-c1015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Mature flowers, field grown plants"
/lab_host="XL10-Gold"
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94.4%;
Score 64.6; DB IV,
Pred. No. 1.2e-10;
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                                                             Length 540;
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Query Match Best Local

Matches

1 Similarity 67; Conserv

Conservative

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Gaps

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 for further information call: (800) 430-0030 or (314) 427-322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine Washington University Box 8501, St. 7444 Forest Park Parkway, Box 8501, St. 7
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ID: Gm-c1074-2145 5' similar to TR:Q9SVI4 Q9SVI4 ES43 LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Public Soybean EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker R/Public Soybean EST Project
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for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XNoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally
                                                                                                                                                                                                                                                            (hypersensitive response) by vacuum infiltrating plant tissue with Pseudomonas syringae pv. glycinea carrying the avrb gene (Genetics 14:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally and 53 hrs after inoculation and their mRNA pooled equally
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1074-2145'
/clone_lib="Gm-c1074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   response)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="seedlings induced for HR (hypersensitive
resnonse)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="9-11 day old"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Query Match Best Local

Matches

1 Similarity 68; Conserv

Conservative

49.98; 86.18;

Pred. No. 1.3e 0; Mismatches Score 61.4; DB 10 Pred. No. 1.3e-09;

DB 10;

Length. 543; Indels

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EST307271 L.
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Lycopersicon
                                                                                                                                                                                                                                                                                             Email:
                                                                                                                                                                                                                                                                                                                             Clemson University
                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
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AW616232
                                                                                                                                                                                                                                                                                       100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                 nitrogen, shearing off trichomes. This procedure yielded mixture of cells which is highly enriched for trichome likely with minor contaminations of other types of leaf
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                                 likely with minor cells"
                                                                                                       /clone_lib="L. hirsutum trichome, Cornell University"
/tissue_type="trichome"
/dev_stage="mixed stages"
/note="Leaves of various stages were shaken in liquid
                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                               /clone="cLHT1L23"
                                                                                                                                                                                                  /db_xref="taxon:62890"
                                                                                                                                                                                                                 organism="Lycopersicon hirsutum"
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                                                                                                                                                                                          Query Match
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64 cactgactggt 74
                                                                       4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
                                            GTATTGTAAATGTGAGATGCCCTACAACCCTGATGATCTGATGGTTCANTGTGAGGGCTG 498
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BE124753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Agronomy and Plant Genetics University of Minnesota 411 Borlaug Hall, 1991 Upper Buford Circle, Tel: 612 625 5715 Fax: 651-649-5058 Fax: 651-649-5058 Email: vance004@marcon.tc.umn.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE124753 574 bp mrNA EST 07-SEP-200 EST393788 GVN Medicago truncatula cDNA clone pGVN-67F7, mrNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Minnesota name:M261621e TIGR sequence name:MTCCC28TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Carroll P. Vance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESTs from one month old nitrogen-fixing root nodules of Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fedorova, M., Pierson, B.L.,
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                                                                                                                                                                                                                                                                                       155
                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                           /note="Vector: pBluescript SK.; Site_1: EcoRI; Site_2: XhOI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meilloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti" /lab_host="E. coli strain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="pGVN-67F7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="N2-fixing root nodules"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="GVN"
                                                                                                                                                                 47.8%;
88.7%;
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                                                                                                                                         Score 58.8; DB 10
Pred. No. 8.9e-09;
0; Mismatches 8
                                                                                                                                                                                     DB 10;
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Craven,M.B., Hansen,T.S.,
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                                                                                                           64 cactgactggt 74
                                                                                                                                                          CAGTGACTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.J. From roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name:N255126e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
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AW586761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; mixed EST libraries.
1 (bases 1 to 514)
                                                                                                                                                                                                                                                                               Similarity
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Tel: 580-223-5810
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Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualifiers
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                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK:, Site_1: EcoR; Site_2:
/note="Vector: pBluescript SK:, Site_1: EcoR; Site_2:
/note="Vector: pBluescript SK:, Site_1: EcoR; Site_2:
/note-"Vector: pBluescript SK:, Site_1: EcoR; Site_2:
XhOI: CDNA was prepared from polya+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-incoulation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
35 a 101 c 127 g 151 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
                                                                    485
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/clone="рмнАм-55G12"
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library"
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                                                                                                                                                                                                                                                                               47.38;
88.78;
                                                                                                                                                                                                                                                       Score 58.2; DB 10;
Pred. No. 1.4e-08;
0; Mismatches 8;
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                                                                                                                                                                                                                                                                                                                                      63;
AW584723 635 bp mRNA EST
N210838e MHAM Medicago truncatula/Glomus ven
Library cDNA clone MHAM-7K19, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: varce004@maroon.tc.umn.edu
Email: varce004@maroon.tc.umn.edu
University of Minnesota name: M271969e TIGR sequence
MTKAK29TK More information is available at:
http://chrysle.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department of Agronomy and Plant Genetics University of Minnesota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBluescript SK +/-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old
plants harvested 36 hours post shoot removal and nodules
collected from 2 month old plants at mid-pod stage"
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/cultivar="genotype A17"
/db_xref="taxon:3880"
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                                                                                                                                                                                                                                                                                            cactgactggt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                           AW584724 655 bp mRNA I
N210839e MHAM Medicago truncatula/Glomus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mjharrison@noble.org
Other name: MHAM-7a-F10; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; Wore information is
available at __'http://chrysie.tamu.edu/medicago'.
Medicago truncatula/Glomus versiforme Eukaryota; mixed EST libraries.
                   Medicago truncatula/Glomus versiforme mixed Medicago truncatula/Glomus versiforme mixed
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Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.,
ESTs from roots of Medicago truncatula after colonization with
                                                                                                                        library cDNA clone MHAM-7K21, mRNA sequence.
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580-221-7380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 day.
post-inoculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_bost="B. colistrain XLOLR"
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/db_xref="taxon:119092"
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                                      EST.

Medicago truncatula/Glomus versiforme mixed EST library.

Medicago truncatula/Glomus versiforme mixed EST library

Medicago truncatula/Glomus versiforme mixed EST library

Eukaryota; mixed EST libraries.

1 (bases 1 to 682)

Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D.,

Rowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.

Rowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.
                   ESTs from roots of Glomus versiforme
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The Samuel Roberts Noble Foundation

OK

Parkway, Ardmore, OK
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Other name: MHAM-7a-F11; Date: 3/14/00; Updated to the Database
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at http://chrysie.tamu.edu/medicago'.
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                                                                                                                                                                                                                                                                       library cDNA clone MHAM-7J12, mRNA
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/dev_stage="Roots harvested at 10, 17, 22, 31 and 38
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/clone="MHAM-7K21"
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              Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                            BG551127 491 bp mRNA EST 09-APR-2001 sad33f01.y1 Gm-c1074 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1074-2162 5' similar to TR:Q9SVI4 Q9SVI4 ES43 LIKE PROTEIN
                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                 Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK
                                                                                                                                                                                                                                                                                                                                  EST
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Soybean EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="roots colonized with Glomus versiforme" /dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages." /lab_host="E. colistrain XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."
172 c 115 g 183 t
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/clone="MHAM-7J12"
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/db_xref="taxon:119092"
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88.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
  Lycopersicon esculentum
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EST244450 tomato ovary,
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                  AI486129.1
                                                                                      AI486129
                                                                                                     cLED5K16, mRNA sequence
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                          tomato.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         info@genomesystems.com web site:
High quality sequence stop: 421.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for cDNA construction. The library was prepared using the Stratagene pBluescript II SK(+) library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with an XhoI restriction site. EcoRI adaptors were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA insert is protected from XhoI digestion via methylation during first strand synthesis. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into E.coli ElectroMax DHIOB host cells. Plant care, inoculations, and library construction were performed by Steve Clough (Lila Vodkin lab, University of Illinois)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"Vector: pBluescript II SK+; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from mRNA isolated from 9-11 day old seedlings that were induced for HR (hypersensitive response) by vacuum infiltrating plant tissue with Pseudomonas syringae pv. 9lycinea carrying the avrB gene (Genetics 141:1597-1604). Plant tissue (expanded unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36, and 53 hrs after inoculation and their mRNA pooled equally
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/db_xref="taxon:3847"
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/lab_host="DH10B"
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/clone_lib="Gm-c1074"
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                   Clemson University
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Email: http://www.genome.clemson.edu/orders/index.html
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                                                                              , Liang, F., Upton, J., Craven, M.B., Bowman, C.L., ,C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. & Generation of ESTs from tomato callus tissue
                                                                                                                                                                                                                                                Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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S.D. and Giovannoni,J.

Generation of ESTs from tomato carpel tissue

'''' had (1999)
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Clemson University Genomics Institute
                              Contact: CUGI
                                                  Unpublished (1999)
                                                                                                                                                               Alcala, J., Vrebalov, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and 3' ends
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/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF'"
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/cultivar="TA496"
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/clone="cleD5K16"
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Pred. No. 4.1e-08;
0; Mismatches 9;
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                                                                                                                                                               White, R., Matern, A.L., Vision, T.,
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Clemson,

SC 29634, USA

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JOURNAL COMMENT
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                                                                                                                                                                                                                                                                                                                                                                          van der Hoeven,R., Sun,H., Bezzerides,J.,
Ronning,C. and Tanksley,S.
Generation of ESTs from Tomato Suspension
                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                                                                                         Clemson University
                                                                                                                                                                                                                                                                                                                          Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                              Contact: CUGI
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                                                                                                                                                                                                                                                                    Jordan Hall, Clemson, SC 29634, USA
ll: http://www.genome.clemson.edu/orders/index.html
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/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Suspension cultures of L.esculentum E6203 were grown in Murashige and Skoog based medium, supplemented with 15% coconut milk (filter sterilized and added after autoclaving), 2% saccharose, and lmg/ml 2,4D (pH5.8). Fresh medium was added every 7 days, and cultures were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xhol; supplier: Giovannoni laboratory; cLEC - Cotyledons of seedlings 7-10 days post-germination were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library" a 149 c 147 g 154 t
                                                                                                                                                             /cultivar="TA496, E6203"
/db_xref="taxon:4081"
/clone="cTOS1768"
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                                                                                                           /tissue_type="suspension cultures"
/lab_host="SOLR"
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/clone_lib="tomato callus, TAMU"
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/db_xref="taxon:4081"
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                                                                                                                                                                                                                                                    ocation/Qualifiers
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cTOS17G8 5'
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Query Match
Best Local Similarity
511 GTACTGTAAATGTGAAATGCCATACAATCCTGATGACCTCATGGTTCAATGTGAGGGCTG
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                     4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg
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Solanum tuberosum
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1 (bases 1 to 732)
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EST513330 CSTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generations of ESTs from dormant potato tubers Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van der Hoeven, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG887479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Cathy Ronning
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                                                                                                                                                                                             /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were store for one month post-harvest at 4oC. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."
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                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="dormant tuber"
/dev_stage="one month post-harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="cSTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="cSTD5N3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism⇒"Solanum tuberosum"
/cultivar="Kennebec"
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                                                                             Score 56.6; DB 11;
Pred. No. 4.8e-08;
0; Mismatches 9;
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Pred. No. 4.7e-08;
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                                                                                                                      DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ewing, E., Cho, J., Chiemin Tanksley, S. and Baker, B.
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                                                                                                                                                                                                                                                                                                         Tubers were stored
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                                                                                                                                                                                                                                                                            52
                                                                                                                                                                                                                                       64 cactgactggtaagtttcacatgtaaggtg 93
                                                                                                                                                                                                                                                                                           4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg 63
                                                                                                                                                                                                         CAAGGACTGGTTCCATCCATCTTGCATGTG 141
                                                                                                                                                                                                                                                                          GTATTGCAAATGTGAGATGCCATACAACCCTGATGACCTCATGGTGCAGTGCGACGCTTG 111
                                                                                                                                                                                                                                                                                                                                           69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence.
BG048538
                                                                                                  BE037301 674 bp mRNA mp19C11 MP Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502,
Mesembryanthemum crystallinum
                                                                    BE03730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG048538 541 1
OV1_14_H02.g2_A002
               common ice plant
                                                  BE037301.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG048538.1
EST.
                                                                                    like protein, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                139
                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Ovary 1 (OV1)"
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Mix of ovaries of varying immature stages
/note="Organ: Display: Incompared by mass adde incompared RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

111 c 141 g 150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Sorghum bicolor"
/db_xref="taxon:4558"
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76.78;
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                                                                                                                                                                                                                                                                                                                                           Score 56.4; DB 11;
Pred. No. 5.3e-08;
0; Mismatches 21;
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threshold for highest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caggtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgaggg 60
                                                                                                                                                                                                                                            l (bases 1 to 959)
Bohnert, H. J., Borchert, C., Brazille, S., Brooks, J.,
H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE039612 959 bp
OC01G11 OC Oryza sativa
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., ,H., Kawasaki, S., McCollough, A., Michalowski, C.B., Scara, G., Wheeler, M. and Zepeda, G.R. Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicott; core eudicott; Carryophyllidae; Carryophyllales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 674)
                                                                                                                                            Tel: 520-621-7982
Fax: 520-621-1697
                                                                                                                                                                                 Bio Sciences West room 513,
                                                                                                                                                                                                 University of Arizona
                                                                                                                                                                                                                    Contact: Michalowski, C.B.
                                                                                                                                                                                                                                  Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE039612.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE03961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bio Sciences West room 513, Tel: 520-621-7982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Michalowski, C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                          Insert Length: 1
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                                                                                   cbm@u.arizona.edu
Length: 1    Std Error:
    Location/Qualifiers
/db_xref="taxon:4530"
/clone_lib="OC"
                                   /organism="Oryza sativa"
/strain="Pokkali"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="apical meristem
/dev_stage="6 weeks"
/note="3 d 500mm NaC1"
184 c 164 g 155 t
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/db_xref="taxon:3544"
/clone_lib="MP"
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NO. 1.8e-07;
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Palacio, C.,
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                               GTACTGCAAGTGCGAGATGCCGTATAACCCGGATGATCTAATGGTGCAGTGCGAGGGATG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGACTGGTTCCCCTCCCTTGNATGGGAAT 170
cactgactggtaagtttca
                                                                                                      63;
                                                                                                                                                                                                                                                                                                                                                                                 Email: scloutier@em.agr.ca
International Triticeae EST Coop
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cereal Research Centre, Winnipeg MT CANADA Tel: 204 983 2340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Laro, G.R., Lin, J.J., McGuire, P., Oglhara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M. and Wenzel, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bread wheat.
Triticum aestivum
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SCL074.H01R990724 ITEC
CDNA Clone SCL074.H01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE418763.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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                                                                                                                                                                                                /clone="SCL074.H01"
/clone_lib="ITEC SCL Wheat Leaf Library"
/tissue_type="young leaf"
/tissue_type="young leaf"
/dev_stage="after 24 hour challenge with LR-AVR1"
/dev_stage="after 24 hour challenge with LR-AVR1"
/note="Vector: Lambda ZAP; 1.0 Kbp average insert size."
231 c 248 g 175 t 42 others
                                                                                                                                                                                                                                                                                     /db_xref="taxon:4565"
/clone="scrops contains
                                                                                                                                                                                                                                                                                                                 /organism="Triticum aestivum"
/cultivar="Thatcher_Lr1"
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225 c 271 g
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Pred. No. 3e-07;
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RESULT 22
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                                                                                                                                                                                                                                                                                                   CAAGGACTGGTTCCATCCA 339
                                                                                                                           BG605300 675 bp mRNA EST 16-APR-2001 WHE2331_B03_D05ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2331_B03_D05, mRNA sequence.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea; Triticeae; Triticeum.
                                                                                                                                                                                                                                                                                                                                                                     63;
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                                            Triticum aestivum
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                                                                                                            BG605300
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Plate: 660003 row: H column:
Location/Qualifiers
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855 California Ave, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Walbot V
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660003H05.x1 660 - Mixed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Anther and pollen cDNA library. Directionally sequenced with 5' end at the EcoRI site. Created by Amle Franklin."

a 129 c 113 g 135 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone_lib="660 - Mixed stages of anther and pollen"
/tlssue_type="whole premieotic anthers to pollen shed"
/dev_stage="premieotic anthers to pollen shed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Zea mays"
/cultivar="Ohio43"
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0; Mismatches 16;
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                                                                                                      Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; Solanum;
                                                                                                                                                                                                                                                                               BG643885 726 bp mRNA EST 24-APR-2001 EST512079 tomato shoot/meristem Lycopersicon esculentum cDNA clone CTOF33K11 5' sequence, mRNA sequence.
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             van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
Hansen,C., Ronning,C. and Tanksley,S.
Generation of ESTs from tomato shoot/meristem tissue
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
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The structure and function of the expi
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Unpublished (2000)
                                                                                                                                                                                                          tomato.
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Site_1: ECORI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA ilbrary was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

80 a 172 c 174 g 149 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Wheat pre-anthesis spike cDNA library"/tissue_type="Spike before anthesis"/dev_stage="Adult plant"/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2331_B03_D05"
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BG320550/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                               Agriculture and Agri-food
960 Carling Avenue, Bldg.
Tel: (613) 759-1662
Fax: (613) 759-1701
                                                                                                                                                                                                                                                                                        Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
                                                                                                                                                                                                                                                                                                                                                                                                           Simmonds, J.A., Singh, J.A., Piche, C., Cass, L., A., Harris, L.J., Hattori, J.I., Ouellet, T., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zm03_10h12_A zm03_AAFC_ECORC_cold_str
cDNA clone zm03_10h12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                  Under High Light Intensity
                                                                                                                                                                                                                                                                                                                                                                    Expressed Sequence Tags from Cold-Stressed Maize Seedlings Grown
                                                                                                                                                                                                                                                                                                                                                                                          and Tinker, N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zea mays.
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100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: CUGI
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                     singhja@em.agr.ca.
Location/Qualifiers
                                                                          /organism="Zea mays"
/cultivar="C0328"
/db_xref="taxon:4577"
/clone="Zm03_10h12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xhol; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."

148 c 148 g 201 t
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                    /tissue_type="Leaf, crown"
/dev_stage="4-leaf"
                                                      /clone_lib="Zm03_AAFC_ECORC_cold_stressed_maize_seedlings"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="tomato shoot/meristem"
/tissue_type="shoot/meristem"
/dev_stage="developing shoots from 4-6wks old plants"
/lab_host="SOLR"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lycopersicon
/cultivar="TA496"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="cTOF33K11"
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Pred. No. 5.2e-07
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Matches 63
                                                                                                                                          Query Match
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                            64. cactgactggta 75
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                                                          tgcactgactggtaagtttca 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        upland cotton.
Gossypium hirsutum
Gossypium hirsutum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3307
Fax: 516-344-3407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biology Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Ben Burr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESTs from developing cotton fiber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI731699.1 GI:5050551
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AI731699
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                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   burr@bnlux1.bnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_2: Xho I; Corn seedlings at 4-leaf stage were exposed to low temperature/high light (10cC/700-800uE/m2/s) for 4 days. Plants were grown/treated by J. Simmonds/L. Cass. Library prepared by C. Piche using Stratagene kit." a 100 c 86 g 110 t 22 others
                                                                                                                                                                                                                                                    /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                     /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
/db_xref="taxon:3635"
                                                                                                                                                                                                                         /note="Vector: pBluescript II KS+" 131 c 159 g 192 t
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                                                                                                                                          42.9%;
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77.8%;
                                                                                                                          Score 52.8; DB 10;
Pred. No. 8e-07;
0; Mismatches 12;
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AI759012/c
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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BE123398
BE123398.1 GI:8516673
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946001F06.X3 946 - tassel
                                                 Zea mays
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                                                                                                AI759012.1
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                                                                                                                               CDNA, mRNA
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Plate: 946001 row: F col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            855 California Ave,
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Biological Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Unpublished (1999)
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Walbot, V.
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/note="Organ: tassels; Vector: HybriZAP; Site_1: Ecox
Site_2: XhoI; George Chuck dissected immature tassels
Site_2: XhoI; George Chuck dissected immature tassels
**Atvaccan 1mm and 3mm. Sharon Stanfield prepared the
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library in Hybr12AP. Sample insert size
to 3 Kb with a 1 Kb average."
1 50 c 52 g 48 t
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/dev_stage="just after the
inflorescence development"
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/cultivar="0H43"
/db_xref="taxon:4577"
/clone_lib="946 - tassel primordium
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83.1%;
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                                                                                                                                                                                                                            Brookhaven National Laboratory
Upton, NY 11973, USA
Tel: 516-344-3396
                                                                                                                                                                                                                                                                                                                                Contact: Ben Burr
Biology Department
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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Contact: Walbot V
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                                                                                                                           Fax: 516-344-3407
Email: burr@bnlux1.bnl.gov
Seq primer: T3 Primer.
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Tel: 650 723 2227
Fax: 650 725 8221
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605085 row: F col
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/organism="Gossypium hirsutum"
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/cultivar="Ohio43"
/db_xref="taxon:4577"
/db_xref="faxon:4577"
/clone_lib="605 - Endosperm cDNA library from Schmidt lab"
/clone_type="nucellar, embryo, and endosperm"
/tissue_type="nucellar, embryo, and endosperm"
/dev_stage="10-14 days post-pollination"
/lab_host="DH5(alpha)"
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Plate: 946033 row: B column:
Location/Qualifiers
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Maize ESTs from various cDNA libraries
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Contact: Walbot V
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mays cDNA, mRNA sequence.
BE639441
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE639441.1
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              Similarity
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                                                                                                                                                                                                                                                               /organism="Zea mays"
/cultivar="0H43"
/db_xref="taxon:4577"
/clone_lib="946 - tasse
                                                                                      /note="Organ: tassels; Vector: HybriZAP; Site_1: EcoRI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDl library in HybriZAP. Sample insert size range was 350 to 3 Kb with a 1 Kb average."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Six-day Cotton fiber"
/tissue_type="immature fiber"
/dev_stage="Six days post anthesis"
/lab_host="%XL1-Blue"
/note="Vector: pBluescript II KS+"
162 c 145 g 190 t 1
                                                                                                                                                                                                /dev_stage="just after the transition inflorescence development"
                                                                                                                                                                                       /lab_host="XLOLR"
                                                                                                                                                                                                                                    /tissue_type="tassels"
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Score 50.8; DB 10;
Pred. No. 3.5e-06;
0; Mismatches 12;
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Pred. No. 1
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Schmidt lab
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RESULT 3
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BF474495
BF474495.1 GI:11543677
                                                                                                                                                                                                                                                           66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A. An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence start: 8 High quality sequence stop: 680.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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213 c 214 g 211 t 1 others
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/clone="GA_Eb0024E17F4"
/clone_1b="GOssyptum arboreum 7-10 dpa fiber library"
/cissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gossypium arboreum"
/strain="AKA"
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KEYWORDS
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 699)
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
RADO Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    wnuerson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., H, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.
The structure and F. J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The structure and function of the expressed genomes - Vernalized crown cDNA library
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Anderson, O.D., Chao, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 81. 58; Conservative
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                                                                                                                                                                                                                                              mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Wheat vernalized crown cDNA library"
/tissue_type="Crown tissue of seedling"
/dev_stage="Five-week old seedling"
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/db_xref="taxon:4565"
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/ta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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81.7%;
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Pred. No. 5.5e-06;
0; Mismatches 13;
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                                                                                         Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                             1 (bases 1 to 861)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yv., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                     BG300821.1 GI:13098348
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG300821 861 bp mRNA EST 22-FEB-2001
HVSMEB0018I16f Hordeum vulgare seedling shoot EST library
HVCDNA0002 (Dehydration stress) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                         Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 634.
                                                                                                                                                                                    for barley genomics
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                            EST
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National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2,
305-8602, Japan ...
                                                                                                                                                      Clemson University Genomics Institute
                                                                                                                                                                       Contact: Wing RA
                                                                                                                                                                                                                  Development of a genetically and physically anchored
                                                                                                                                                                                                                                       Wood, T.
                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                                                                                                                                                                                                                                                            barley.
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Fax: 81-298-38-7468
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Rice cDNA from panicle at ripening stage (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
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/strain="Nipponbare"
/db_xref="taxon:4530"
/clone="E10910"
                              Location/Qualifiers
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/dev_stage="ripening stage"
/note="Organ: panicle; Rice cDNA from panicle at ripening
/organism="Hordeum vulgare"
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339 CAAAGACTGGTTCCATCCA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khann, A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers, Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurl,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW459464 420 bp mRNA EST 17-JUL-2000 sh41e10.yl Gm-c1017 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1017-4291 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                    This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                                                                                                                                                                                Insert Length: 451 Std Erro
Seq primer: -40RP from Gibco
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                                                                                                                                                                                                                                                                           info@genomesystems.com web site: www.genomesystems.com
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more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
a 209 c 230 g 197 t 3 others
/clone="GENOME SYSTEMS CLONE ID: Gm-c1017-4291"
/clone_lib="Gm-c1017"
                                                           /organism="Glycine max"
/db_xref="taxon:3847"
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/clone="HysMEb0018116f"
/clone_lib="Hordeum vulgare seedling shoot EST library
/HYCDNA0002 (Dehydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TJC121"
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RESULT 36
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: radixon@noble.org
Insert Length: 539 STA Error: 0.00
Plate: 098 row: E column: 01
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Erpelding."
74 c
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/lab_host="XLIO-Gold"
/note="vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolate
from vegatable buds of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
                                  /clone_lib="Elicited cell culture"
/tissue_type="Cell cultures derived from root tissues"
/dev_stage="Cell suspensions were subcultured every 14
days. Cells were induced six days after subculture"
                                                                                                                                                                                                                                    /clone="NF098E01EC
                                                                                                                                                                                                                                                                                          /db_xref="taxon:3880"
/note="Vector: Lambda Zap; Cells were induced with yeast
                                                                                                                                                                                                                                                                                                                                /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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Pred. No. 7.9e-06
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 gcactgactggt 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaa-tgcgagggct 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCANTGACTGGT 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US Department of Agriculture, Agriculture Research US Department of Agriculture, Agriculture Research West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BG605406 586 bp mRNA EST 16-APR-2001 WHE2329_E06_I11zS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2329_E06_I11, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 586)
Anderson,O.D., Chao,S., Choi,D.W., Clo,P.S., Hsia.C.C., Kang,Y., Lazo,G.R., Seaton,C.L. and Tong,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Triticum aestivum
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                     poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                            /Clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coll SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation. 108 c 125 g 157 t 3 others
                                                                                                                                                                                   greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
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pred. No. 9.7e-06;
"" matches 7;
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a; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khann, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.
Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurl, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3225 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert Length: 1604 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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sa30h05.yl Gm-c1004 Glyc
Gm-c1004-850 5' similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYA-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
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314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    quality sequence stop: 417
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/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; Root cDNA. The mRNA was isolated from entire roots of 8 day old 'Williams' seedlings which were propagated on paper towels with distilled water. Stratagene's cDNA synthesis Kit (catalog #200401) was used to synthesize the cDNA. First- strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA is hemimethylated. Stratagene's first-strand synthesis primer was used [GAGAGAGAGAGAGAGAGAGAGAGTGTCTGGAG(T)-18]. After second-strand synthesis, the cDNA ends were 'polished' with clone Pfu DNA polymerase, ligated to EcoRI adapters,
                                                                                                                                                                                                                                                                                      /clone_lib="Gm-c1004"
/tissue_type="root"
/lab_host="XL10-Gold"
                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th: 1604 Std Error: -40RP from Gibco
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80.3%;
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Pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;, mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272 CAAGGATTGGAAA 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 gtattgtaaatgtgagatgccttacaaccctgatgacctaatggcgcaatgcgagggctg 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LO-529T3 Ice plant Lambda Uni-Zap XR expression library, O hour NaCl treatment Mesembryanthemum crystallinum cDNA clone LO-529 similar to receptor-like protein, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                   Plate: L0-6
                                                                                                                                                                                                                          BACKWARD:
                                                                                                                                                                                                                                                                                                                                              MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                              Department of Biochemistry
University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesembryanthemum crystallinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cushman, J.C
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                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                                                            Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          An expressed sequence tag database for the common ice plant
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                                                                                                                                                                         primer: T3
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                                                                                                                                               quality sequence stop: 340
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                                                                                                                                                                                                                                                                                                  jcushman@unr.edu
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                                                   /organism≃"Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
                         /clone="L0-529"
                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                          Τ3
/clone_lib="Ice plant Lambda Uni-Zap XR expression library
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                                                                                                      . 380
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79.5%;
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ches 15;
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                                                                                                        Local Similarity hes 57; Conserv
                         64
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                                                cactgactggt 74
TAAAGACTGGT 488
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AU084649.1
EST.
                                                                                                                                                                                                                                                                                                                                          Cryptomeria japonica
Plant Mol. Biol. 43, 451-457 (2000)
Contact: Tokuko Ujino-Ihara
Bio-resources Technology Division
Porestry and Forest Products Research Institute
Matsunosato 1, Kukizaki, Ibaraki 305-8687, Japan
Tel: 81-298-73-3211(ex.444)
Fax: 81-298-73-3795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cryptomeria japonica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AU084649 490 bp mRNA E AU084649 Cryptomeria japonica inner bark clone CC1649 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                   Email: udino@ffpri.affrc.go.jp;
URL:http://www.ffpri.affrc.go.jp/labs/cjgenome/database/cjdatae.htm
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ujino-Ihara,T., Yoshimura,K., Ugawa,Y., Yoshimaru,H., Nagasaka,K. and Tsumura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression analysis of ESTs derived from the inner bark of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cryptomeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Japanese cedar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Leaf"
/dev_Stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
ECORI; Site_2: XhoI"
a 69 c 96 g 113 t
                                                                                                                                                                                   /organism="Cryptomeria japonica"
/db_xref="taxon:3369"
/clone="CC1649"
/clone_lib="Cryptomeria japonica inner bark"
/tissue_type="inner bark"
/tissue_type="inner bark"
99 c 141 g 115 t
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hes 14;
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                                                                                                                                                                       64 cactgactggt 74
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Unpublished (2001)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
AW448025 658 bp mRNA EST 03-JAN-2001
BRY_1261 BRY Triticum aestivum cDNA clone P28-2A, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                  l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton Anderson,O.D., Chao,S., Chin,A., Close,T.J., Doherty,L., Fenton R.D., Lazo,G.R., Rausch,C.J., Walker-Simmons,M.K. and Wilson,C. The structure and function of the expressed portion of the wheat genomes - Dormant embryo cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG606610 558 bp mRNA EST 17-APR-200: WHE2958_F12_L242S Wheat dormant embryo cDNA library Triticum aestivum CDNA clone WHE2958_F12_L24, mRNA sequence.
BG606610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence with phred score less
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
/inote="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: XhOI; Plants were grown to seed
maturity under conditions favoring seed dormancy (L.
Dohery at K. Walker_Simmons lab, Washington State
University, Pullman, WA). Embryos were cut from mature
dormant seed (Doherty). Total RNA was prepared from these
embryos, polyA was purified, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab at the University of
California, Riverside (Chin, Fenton). Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

62 a 115 c 149 g 131 t 1 others
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/dev_stage="Mature seed"
/lab_host="E. coli SOLR"
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/clone_lib="Wheat dormant
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les 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTGATTGGT 593
                                                                                         Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                              BE346433 594 bp mRNA EST 18-JUL-2000 sp25e05.yl Gm-c1042 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1042-1593 5' similar to TR:065462 065462 RECEPTOR LIKE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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BE346433.1 GI:9258286
EST.
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Division of Plant Industry
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                                                                             Unpublished (1999)
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/clone="P28-2A"
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186 c 176 g
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HV_CEb0003J01f Hordeum vulgare seedling green leaf EST library
HVcDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57;
                                                                                                                                                                                    Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVCDNA0005 (Erysiphe
HV_CEb0003J01f, mRNA
BE214475
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This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
Parkway Circle St. Louis, Missouri 63134 For further information
Call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                          Contact: Wing RA Clemson University Genomics Institute
                                                                                       Development of a genetically for barley genomics Unpublished (2000)
                 Clemson University
                                                                                                                                                                   Wood, T.
                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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100 Jordan Hall,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 79.: 57; Conservative
                                                                                                                                                                                                                                                                                         Triticeae; Hordeum.
                                                                                                                                                                                                                                                                (bases 1 to 706)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from 2 week old seedlings with the cotyledons removed at the time of harvest. The seedlings for the cultivar Raiden were grown in a growth chamber using germination paper. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This
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/db_xref="taxon:3847"
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/lab_host="DH10B"
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/clone_lib="Gm-c1042"
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2.8e-05;
15;
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BE519330
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                                                                                                                                                                                                                  Contact: Walbot v
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbottstanford.edu
Plate: 945023 row: A column: 05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SK) Zea mays cDNA, mRNA sequence.
BE519330
BE519330.1 GI:9743182
EST.
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Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE519330 444 bp mRNA
945023A05.y1 945 - Mixed adult tissues
                                                                                                                                                                                                                                                                                                                                                                                                      University
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Maize ESTs from various cDNA libraries sequenced at Stanford
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/clone_lib="945 - Mixed adult tissues
same as 707 (SK)"
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/tissue_type="seedling green leaf"
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Pred. No. 2.9e-05;
0; Mismatches 20;
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> 124 a Vector: pGAD10; Site_1: ECORI; cDNA library from fully differentiated maize tissues from an active Mutator plant. Tissue ratio is 4:2:1:1:1:1 (tassel, kernel, silk, husk, root, leaf). Unidirectionally cloned. New library number given to library 707 for additional sequencing." 95 c 109 g 116 t plant.

ORIGIN BASE COUNT

QΥ Matches Query Match Best Local : Local Similarity 56; Conservative 38.2%; 78.9%; 0; Score 47; DB 10; Pred. No. 5.6e-05; Mismatches 15; Length 444; Indels Gaps

0,

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밁 Qy 297 TTCTGACTGGT 307 64 cactgactggt 74

Search completed: March 19, 2002, 10:18:40 Job time: 2754 sec

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180 601 66 288

pathway;
promoter;

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Sequence

Strd Orig

ZSCOTE

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Query length: 123
Database: A_Geneseq_1101:*
Database sequences: 522463
Database length: 74073290
Search time (sec): 29.300000
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Copyright (c)
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99US-0157117

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seq_documentation_block:
ID          AAB93780 standard; Protein; 790 AA
XX
AC          AAB93780;
XX
DT          26-JUN-2001 (first entry)
XX
DE          Human protein sequence SEQ ID NO:1
XX
KW          Human; primer; detection; diagnosi
XX
OS          Homo sapiens.
XX
PN          EP1074617-A2.
                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAB93780
                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAG40193
                                                                                                                                                                                                                                                                                            US-09-684-016-48411 x AAG40193
                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
                                                               Human protein sequence SEQ ID NO:13511.
                                                                                                                                                                                     296
                                                                                                                                                                                                                            280 PheCysLysCysGluMetProTyrAsnProAspAspLeuMetValGlnCy 296
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                                                                                                                                                                                                                                      TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
                                                                                                                                                                                                       CGAGGGCTGCACTGACTGG
                                                                                                                                                                                   sGluGluCysSerGluTrp 302
                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                       Ratio:
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
                                          detection; diagnosis; antisense therapy; gene therapy.
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99US-0160981.
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99US-0160815
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99US-0160770.
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99US-0160767.
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99US-0158029
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5.636
95.652
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                                                                                                                                                                                                                                                                                                                           Percent Identity: 78
                                                                                                                                                                                                                                                                       to:
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0
.261
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises as sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary strand of a polynucleotide which comprises a 5'-end complementary to a sequence complementary to a sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a coligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the coligonucleotide comprises a 3'-end sequence, where the specification. The primers set useful for synthesising polynucleotides in gene therapy. The primers are useful for synthesising polynucleotides, comparisonally full-length cDNAs. The primers are also useful for the capacition and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers also wobtaining of the full-length cDNAs. The primers also wobtaining of the full-length cDNAs easily without any specialised methods. AAH33168 to AAH3628 and CC AAH35833 to AAH38742 represent human capacities; and AAH33629 to AAH3633 co represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 13511; 2537pp + CD ROM; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sogai T, Nishikawa
Sugiyama T, Wakama
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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  AA;
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Wakamatsu
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A, Nagai K,
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Otsuki
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alignment_block:
US-09-684-016-48411 x AAB93780
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                                                                                                              Align seg 1/1 to: AAB93780
                                                                                                                                                                                   Ratio:
Percent Similarity:
 23
                          55
              CGAGGGCTGCACTGACTGG 73
                                                     TyrCysLeuCysArgLeuProTyrAspValThrArgPheMetIleGluCy 23
                                                                                   TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
sAspMetCysGlnAspTrp
                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                   74.00
4.625
69.565
 29
                                                                                                                from: 1
                                                                                                                                                                         Length: 23
Gaps: 0
Percent Identity: 43.478
                                                                                                                to:
                                                                                                                790
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seq_documentation_block:
ID AAB42371 standard; Protein; 1084 AA.

seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB42371

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antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, praft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus artificiants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999;
02-APR-1999;
05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipscriatic, antipscriatic, activities such as:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
                                                  erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, altergies, aplastic anaemia, burns, wounds, bone and cartilage damage nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                              antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vulnerary; antipsoriatic; antiparkinsonian;
anticonvulsant; osteopathic; antiarthritic;
                                                                                                                                                                                                                                                                                                        immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
antidiabetic; hypotensive; dermatological; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                              AAC74446 to AAC77606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimkets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000;
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DB; AAC76580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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99US-0127636.
99US-0127728.
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immunosuppressant;
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                                                                                                                                                                                                                                      21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; thrombolytic; drug screening; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   documentation_block:
        The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                      Novel nucleic acids and such as central nervous
                                                                                                                                                  Zhao
                                                                                                                                                                   Tang
                                                                   Example
                                                                                                                    N-PSDB;
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                                                                                                                                                                                                                                                                                                                                       WO200153312-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAM40982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM40982 standard; Protein;
                                                                                                                                                                                      (HYSE-)
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DB; AAI60138.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide
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                                                                   2;
                                                                                                                                                                                      HYSEQ INC
                                                                                                                                                Liu C,
Wang Z,
Zhou P,
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2000US-0552317.

2000US-0598042.

2000US-0620312.

2000US-0653450.

2000US-0693036.

2000US-0693036.

2000US-0727344.
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                                                                    IJ
peripheral
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4.625
69.565
                                                                    Ö
                                                                                                                                                          Asundi V,
Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO
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                                                                   5913;
                                                                                      polypeptides,
system injuri
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                                                                 10078pp;
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Xu C,
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43.478
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Yang Y,
peripheral
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Zhang
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                                                                                                 disorders
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                                                                                                                                                          J,
                                                                                                                                                                   Wang
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seq_documentation_block:
ID AAM39196 standard; P:
XX AAM39196;
XX AAM39196;
XX Human polypeptide SEC
XX Human; nootropic; imm
KW Human; nootropic; imm
KW Alzheimer's; Parkinso
KW Alzheimer's; Parkinso
KW Alzheimer's; Parkinso
KW Alzheimer's; Parkinso
KW Alzheimer's; Parkinso
KW Chemokinetic; thrombo
KW Leukaemia.
XX Chemokinetic; thrombo
KW Chemokinetic; thrombo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAM40982 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-684-016-48411 x AAM40982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemothetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 2341.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OASpGluMetIleGlnCysValValCysGluAspTrp 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TyrCysIleCysLysArgProTyr...ProAspProGluAspGluIlePr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATTGTAAATGTGAGATGCCTTACAACCCTGAT.........
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:AAM39196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 425 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
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2000US-0598042
2000US-0620312
2000US-0653450
2000US-0662191
2000US-0693036
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                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725
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4.433
51.724
                                  Asundi V, Ch
Wehrman T, 7
Goodrich R,
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                                                                                 Chen R,
                                                                 Χu
                                  u C, Xue
Drmanac R
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Gaps: 2
t Identity: 48.276
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                  Ma Y,
Xue AJ,
RT;
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                                                              Qian XB,
Yang Y,
                                                              Zhang J;
                                                                                             Ren F,
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                                                                                          Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer;
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seq_documentation_block:
ID AAB60498 standard; PR
XX
AC AAB60498;
XX
24-APR-2001 (first e
XX
DT 24-APR-2001 cycle and
DE Human cell cycle and
XX
Cell cycle and prolli
KW antagonist; gene thei
KW transgenic animal disord
KW developmental disord
KW cell proliferative di
KW arteriosclerosis; asi
KW arteriosclerosis; asi
KW arteriosclerosis; asi
KW arteriosclerosis; asi
XX
OS Homo sapiens.
XX
PN W0200107471-A2.
XX
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-L
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypurucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                   transgenic animal disease model; immune disorder; developmental disorder; cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  utilisation of the activities such as: Immune system suppression, activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
                                                                                                                                                                                              menstrual cycle disorder; bacterial infection.
                                                                                                                                                                                                                      arteriosclerosis; asthma; allergy;
                                                                                                                                                                                                                                                                                                 Cell cycle and proliferation protein; CCYPR; human; antagonist; gene therapy; detection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                 Human cell cycle and proliferation protein CCYPR-46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB60498 standard; Protein; 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 TyrCysIleCysLysArgProTyr...ProAspProGluAspGluIlePr 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; SEQ ID NO 2341; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI58352.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   {\tt oAspGluMetIleGlnCysValValCysGluAspTrp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATTGTAAATGTGAGATGCCTTACAACCCTGAT........
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The sequence data for this patent did not form
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: AAM39196
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                          2000WO-US19948
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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4.433
51.724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to:
                                                                                                                                                                                                                      diabetes mellitus;
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2
48.276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             part of the printed
                                                                                                                                                                                                                                        epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
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seq_documentation_block:
ID AAG47973 standard; Protein; 193 AA
XX
AC AAG47973;
XX
AC AAG47973;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragm
XX
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US-09-684-016-48411 x AAB60498
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunosasys to detect CCYPR. CCYPR itself may be used to detect Ccompounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to Cidentify compounds that modulate the activity of CCYPR. CCYPR compounds that modulate the activity of CCYPR. CCYPR concleotides can be used to generate transgenic animal models of human concleotides and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR for the creatment or prevention of a disorder associated with CCYPR. CCYPR concleotides with can be diagnosed, treated and prevented using CCYPR proteins, nucleic acids, agonists or antagonists include immune, concertions, nucleic acids, agonists or antagonists and cell proliferative disorders including cancer. Specific examples of these disorders include anaemia, aphileps, arteriosclerosis, asthma, cancer, allergies, alterators of the menetry and infertions.
                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAB60498 from: 1
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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08-SEP-1999;
10-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequences AAB60453-AAB60506 represent 54 human cell cycle and proliferation proteins (CCYPR), which are encoded by AAF59590-AAF59643. CCYPR and agonists of CCYPR are used to treat discases or conditions associated with decreased expression of functional corpe, while CCYPR antagonists are used to treat diseases or conditions associated with overexpression of functional CCYPR. Monoclonal or polyclonal antibodies
              Arabidopsis thaliana protein fragment SEQ ID NO: 60527
                                                                                                                                                                           149
                                                                                                                                                                                                                              134 TyrCysIleCysLysArgProTyr...ProAspProGluAspGluIlePr 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 156-157; 205pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signaling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used
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N-PSDB; AAF59635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                      38
                                                                                                                                                                                                                                                               5
                                                                                                                                                                          oAspGluMetIleGlnCysValValCysGluAspTrp 161
                                                                                                                                                                                                                                                            TATTGTAAATGTGAGATGCCTTACAACCCTGAT.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n cell cycle and proliferation proteins and polynucleotides are to treat, diagnose and prevent immune, developmental and cell aling disorders and cell proliferative disorders including cancer
                                                                                                                                                                                                      .GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGG
                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAG47973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   425
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Yang J,
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99US-0153129.
99US-0164647.
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4.433
51.724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disorders of the menstrual cycle and infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT
                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 48
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Baughn MR,
                                                                                                                                                                                                                                                                                        to: 425
                                                                                                                                                                                                                                                                                                                                                                             Length:
Gaps:
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R, Patterson
                                                                                                                                                                                                                                                                                                                                                              29
2
. 276
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C, Shah P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allergies,
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
                                                 promoter;
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Arabidopsis thaliana

EP1033405-A2

25-FEB-2000; 06-SEP-2000 2000EP-0301439

25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 23-MAR-1999; 25-MAR-1999; 29-MAR-1999; 01-APR-1999; 06-APR-1999; 99US-0126264. 99US-0126785. 99US-0127462. 99US-0128234. 99US-0128714. 99US-0123180. 99US-0123548. 99US-0125788. 99US-0121825

08-APR-1999; 16-APR-1999; 19-APR-1999; 21-APR-1999; 23-APR-1999; 99US-0130449 99US-0130510 99US-0129845 99US-0130077

23-APR-1999; 28-APR-1999; 30-APR-1999; 30-APR-1999; 04-MAY-1999; 05-MAY-1999; 99US-0132484. 99US-0132485. 99US-0132486. 99US-0132487. 99US-0130891. 99US-0131449. 99US-0132048. 99US-0132407.

06-MAY-1999; 06-MAY-1999; 07-MAY-1999; 11-MAY-1999; 99US-0132863. 99US-0134256. 99US-0134218. 99US-0134219. 99US-0134221.

14-MAY-1999 14-MAY-1999 14-MAY-1999; 99US-0134370 99US-0134768

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                                                                                                                                                                                             Align seg 1/1
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29-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-190585/16.
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                                                   sAspArgCysGlnAsnTrp 83
                                                                                       CGAGGGCTGCACTGACTGG
                                                                                                                      TyrCysIleCysArgThrProTyrAspGluSerGlnPheTyrIleGlyCy
                                                                                                                                                          TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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DT 22-FEB-2000 (first entry)
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KW Human; transcriptional regulatory factor
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CC compounds binding to it and acting
CC cother cell proliferation disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hSNF2H, hSNF2L and NCOA-62/Skip. It can be used for screening
 22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a human transcriptional regulatory factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 139-151; 154pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcriptional regulatory factor containing a bromo domain TCoAl encoding it
                                                                                                                                                                                                          55 CGAGGGCTGCACTGACTGG 73
                                                                                                                                                                                                                                                                                  5 TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
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transcriptional regulatory factor SEQ

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KW Protein identification; signal transdik
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KW Protein sasay; genetic mapping;
XX
CS Arabidopsis thaliana.
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PN termination sequence.
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DE Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                       2730
                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human transcriptional regulatory factor containing a bromo domain. The factor interacts with proteins involved in the chromatin-mediated transcription regulatory mechanism. It binds to hswr2H, hswr2L and NCOA-62/SKip. It can be used for screening compounds binding to it and acting as agonists or antagonists, which are potentially useful for the treatment and prevention of cancer and
                                                                                                 Arabidopsis thaliana protein fragment SEQ
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N-PSDB; AAZ39032.
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bromo-domain; cell proliferation;
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Human

associated

protein sequence

SEQ ID NO:1169

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alignment_block:
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                                                                                Align seg 1/1
                                                                                                                      US-09-684-016-48411 x AAB43724
                                                                                                                                                                                     Percent
                                                                                                                                                                                                                                                                                                                                                          dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, altergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the cardiovascular disorders and pathological disease and hab44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC//bU/ to AAC/8448 encode the human cancer associated proteins gi
in AAB43398 to AAB44239. The proteins can have activities based on
tissues and cells the genes are expressed in. Example of activities
                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         include: cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC77607 to AAC78448 ence
in AAB43398 to AAB44239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 1790-1791; 2352pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - {\sf cancer}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dermatological; neuroprofective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiatrhitic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
26
                                        U
TyrCysIleCysArgGlnProHisAsn..
                                     TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG
                                                                                                                                                                                   Similarity:
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                                                                                AAB43724
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAY67579
             The invention provides nucleic acids encoding the human and murime inducer-obliterator 1 (DIO-1) polypeptides. The polypeptides can be expressed by standard recombinant methodology. The DIO-1 polypeptides, agonists and antagonists are used as medicament for treating diseases characterized by an alteration in cell death or by hyperproliferation, e.g. cancer, autoimmune diseases, diabetes, rheumatoid arthritis, benign tumours, malignant tumours or hyperproliferative skin disorders. They are also useful in the treatment of metabolic, proliferative or inflammatory also useful in the treatment of represents the human DIO-1 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _documentation_block:
AAY67579 standard; Protein;
                                                                                                                                                                                          New DNA encoding human and murine death inducer-obliterator 1 polypeptides, useful in the treatment of cancer, autoimmune diseases diabetes, rheumatoid arthritis, benign tumors, malignant tumors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Death inducer-obliterator 1; DIO-1; cell death; cancer; tumour; autoimmune disease; cytostatic; immunosuppressive; antidiabetic; antirheumatic; antiinflammatory; antiproliferative.
Sequence
                                                                                                                                                       Claim
                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                      Alonso
                                                                                                                                                                               hyperproliferative skin disorders
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17-SEP-1998;
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DB; AAZ90578.
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  562 AA;
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98US-0100873.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .320
                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "zinc finger motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence"
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                                                                                                                                                                                                                                                                                      Martinez
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alignment_scores:

Quality: Ratio:

56.50 3.531 69.565

Percent

Identity: Length:

39.130

Percent Similarity:

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seq_documentation_block:
ID AAB93638 standard; Pr
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Human; primer; detect
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29-JUL-1999; 99JP-1
PR 27-AUG-1999; 99JP-1
PR 27-AUG-1999; 99JP-1
PR 27-AUG-1999; 99JP-1
PR 17-AUG-1999; 99JP-1
PR 09-JUN-2000; 2000JP-1
PR 09-JUN-2000; 2000JP-1
PR 09-JUN-2000; 2000JP-1
PR 09-JUN-2000; 2000JP-1
PR 15hii S, Sugiyama T
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Ota T, Isogai T, N
PI Ishii S, Sugiyama T
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CC comprises: (a) an oll
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The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of CC cliponucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC oligonucleotide comprises at least 15 nucleotides and the combination of CC the 5'-end sequence', '-end sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-684-016-48411 x AAY67579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and for the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB93638 standard; Protein; 562
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Sugiyama T, Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 2000JP-0118776.
; 2000JP-0183767.
; 2000JP-0241899.
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A, Nagai K,
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Death inducer-obliterator 1; DIO-1; cell death; cancer; tumour; mouse; autoimmune disease; cytostatic; immunosuppressive; antidiabetic; antirheumatic; antiinflammatory; antiproliferative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                      N-PSDB;
                                                                                                                                                                                   Alonso CM,
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                                                                                                                                                                                                                                                                                                                     10-SEP-1998;
17-SEP-1998;
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                                                                                                                                                                                                                                     (CNSJ ) CONSEJO SUPERIOR INVESTIGACIONES (BANN/) BANNERMAN D G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATG 54
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DB; AAZ90579.
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                                                                                                                                                                                 Domingo DG,
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98US-0100873
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/note= "zinc finger motif"
290..315
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69.565
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162..170
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Gaps:
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39.130
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New DNA encoding human and murine death inducer-obliterator 1 polypeptides, useful in the treatment of cancer, autoimmune diseases, diabetes, rheumatoid arthritis, benign tumors, malignant tumors and

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention provides nucleic acids encoding the human and murine dea inducer-obliterator I (DIO-1) polypeptides. The polypeptides can be expressed by standard recombinant methodology. The DIO-1 polypeptides, agonists and antagonists are used as a medicament for treating disease characterized by an alteration in cell death or by hyperproliferation, e.g. cancer, autoimnune diseases, diabetes, rheumatoid arthritis, beni
                                                                                                                                                                                                                                                                                                                              5-oxoprolinase; rat; glutathione;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW61369 standard; Protein; 1288 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conditions. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumours, malignant tumours or hyperproliferative skin disorders. also useful in the treatment of metabolic, proliferative or infla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Fig 1D;
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Ratio:
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                                        96US-0762428
                                                              97WO-US22851
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698
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919
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1106
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e represents the murine DIO-1 polypeptide
                                                                                                                                                                                          N-glycosylated"
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39.130
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:AAW18030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  In the metabolism of glutathione. The amino acid sequence is deduced from a cDNA sequence (see AAV28112) derived from overlapping clones from a rat kidney cDNA library. The invention is directed toward isolated nucleic acid molecules encoding mammalian 5-oxoprolinase (m50P). Deficiency of this enzyme is associated with 5-oxoprolinuria. Expression vectors and host cells comprising the nucleic acid molecules are provided, as well as methods of increasing (by gene therapy) or decreasing (e.g. using antisense or ribozyme molecules) the expression of m50P in host cells. The invention also provides a method of screening a substance for its ability to modify m50P function, and a method for isolating other m50P molecules. DNA probes and primers, and antibodies specific for m50P are provided, each of which can be used to detect the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 HisValSerLeuSerSerGluValMetProMetValArgIleValProAr 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          catalyses the ATP dependent in the metabolism of glutath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises rat 5-oxoprolinase, an enzyme that catalyses the ATP dependent cleavage of 5-oxoproline to L-glutamate
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N-PSDB; AAV28111-12.
       (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                         Huntingtin interacting protein; HIP1; Huntington's disease;
                                                                                                                                                                                                                                                           Huntingtin interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                              231 gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalian 5-oxoprolinase - useful for developing products treating 5-oxoprolinuria {\sf T}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme in a sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86 CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCCATT 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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                                      95US-0006882.
                                                                       96WO-US18370
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seq_documentation_block:
ID AAY59269 standard; Pr
XX AC AAY59269;
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XX 17-APR-2000 (first e
XX Huntingtin Interactir
XX Huntingtin Interactir
XX Huntingtin S disease;
XX Huntington's disease;
XX Homo sapiens.
XX PN w09960986-A2.
XX PD 02-DEC-1999.
XX 27-MAY-1999; 99WO-1
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US-09-684-016-4
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                                                                                                                                                                                                                                                                                                                                                   Huntingtin Interacting Protein; HIP; death effector domain; DED; human; apotosis; HIP-apoptosis modulating protein; cell death; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of huntingtin into brain cell membranes. Its amino acid sequence was deduced from a human frontal cortex cDNA clone (AAT67187). The effects of HD in a patient expressing huntingtin protein with an expanded polyglutamine tract can be ameliorated by increasing the amount of expressed HIPI in the brain using gene therapy approaches. Modified forms of HIPI which bind more effectively to expanded HD protein can be used to convert the expanded protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human huntingtin-interacting protein (HIP1).
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                                                                                                                                                                                                                                                                                                               disease; nootropic; anticonvulsant; cytostatic;
                 99WO-US11743.
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                                                                                                                                                             17-APR-2000
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                                                                                                                           Human huntingtin-interacting protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   techniques, and cancers
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(MERI ) MERCK FROSST CANADA INC.
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Huntingtin Interacting Protein; HIP; death effector domain; apotosis; HIP-apoptosis modulating protein; cell death; gene Huntington's disease; nootropic; anticonvulsant; cytostatic;

gene

therapy;

chromosome 7q11.23.

Homo sapiens

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KW XXX AC XXX DE XXX DE XXX
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US-09-684-016-48411/rev x AAY59270
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(MERI)
                                                      Human gene 17 encoded secreted protein HTOIZ28, SEQ ID NO:115
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             secreted protein; proliferative disorder; cancer; tumour; abnormality; developmental abnormality; haematopoietic di
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MERCK FROSST CANADA INC.
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              disorder;
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cc 19 genes, based on the tissues in which they are most highly expressed, cand include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental control proliferative disorders, cancer, tumours, foetal and developmental control proliferative disorders, diseases of the immune system, although autoimmune diseases (e.g., rheumatoid arthritis), inflammation, callergies, neurological disorders, although arthritis), inflammation, callergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, atherosclerosis, cardiovascular disorders, angiogenic disorders, kidney disorders, candiovascular disorders, pregnancy related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in a disparent of temperature of primary and with the disorders mentioned above, and
                                                                                                                                                                                                                                                                                                                                                 and inc
                                                                                                                                                                                                                                                                                                                                                                                            The genes and their secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD07705-AAD07759 represent cDNAs corresponding to 19 human secreted protein genes, and AAE03292-AAE03346 represent the proteins they encode. AAE03347-AAE03375 represent human secreted protein fragments or variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preventing, treating or amelioral Parkinson's diseases and cancers
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30-JUN-2000; 2000US-0215128.
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Soxco

secreted protein of the invention

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seq_documentation_block:
ID AAE03308 standard; Pr
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XX Human gene 17 encoded
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KW Immune system disorde
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KW cell culture; chemota
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XX Homo sapiens
XX 10-MAY-2001.
XX 17-MAY-2001.
XX 17-MAY-2001.
XX 17-MAY-2000; 2000WO-U
XX 12-NOV-1999; 99US-0
PR 30-JUN-2000; 2000WS-0
PR 30-JUN-2000; 2000WS-0
PR 11-NOV-1999; 99US-0
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                                                                            12-NOV-1999; 99US-0164750.
30-JUN-2000; 2000US-0215128.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 19 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, hammatogicatic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatogic arthritis), inflammation,
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seq_documentation_block:

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alignment_block:
US-09-684-016-48411 x AAY36128
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                                                                                                                                                                                             Ratio:
Percent Similarity:
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chamatopoiesis.
                                                                                                                                                                                                                                                                                                             or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is encoaed by sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secreted protein; human; cytokine; cellular proliferation; cell movems cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tunour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therap;
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extended human secreted protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY36128 standard;
 85
                              88
                                                            69
                                                                                         38
uPheLeuTyrLeuSerAlaGluTyrSerThrLys
                           AAGGTGATACTTATCTTCAATTTATTCCACACAA 121
                                                     {\tt AspIleThrAlaAspLeuGluAsnIlePheAspTrpAsnValLysGlnLe}
                                                                                      GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-385906/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9;
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                                                                                                                      ťo:
                                                                                                                                                                                                                                                                                     180 AA;
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                                                                                                                      AAY36128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0074121
98US-0081563
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97US-0069957
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2.650
71.429
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                                                            85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell movement;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapy;
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seq_name: /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB24029
ζ
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protein sequence SEQ ID NO:27

diagnosis; neoplastic disease;
; tumourigenesis; anticancer; d detection. proliferation;

ΑL, Roy MΑ, Watanabe CK, Wood ¥,

expression PRO polypeptides, used to diagnose amammals, and to identify inhibitors expression and s of inhibit

226pp; English.

seq_documentation_block:

ID AAB24029 standard; Protein; 180 AA

XX

AC AAB24029;

XX

DT 25-JAN-2001 (first entry)

XX

DE Human PR03567 protein sequence SEQ

XX

Human; tumour; diagnosis; neoplast

KW Human; tumour; diagnosis; neoplast

KW Human; tumour; diagnosis; neoplast

XX

Homo sapiens.

XX

PN

W0200053750-A1.

XX

14-SEP-2000.

XX

02-DEC-1999; 99WO-US2851.

PR

01-SEP-1999; 99WO-US28131.

PR

01-DEC-1999; 99WO-US28634.

XX

O2-DEC-1999; 99WO-US28634.

XX

O3-NOV-1999; 99WO-US28634.

XX

PR

01-DEC-1999; 99WO-US28634.

XX

AGETH ) GENENTECH INC.

XX

BOTSTEIN D, Goddard A, Gurney AI

XX

RPI; 2000-594320/56.

PR

WPI; 2000-594320/56.

DR

WPI; 2000-594320/56.

PR

WPI; 2000-594320/56.

PR

WPI; 2000-594320/56.

DR

N-PSDB; AAC58111.

XX

AGETH ) GENENTECH INC.

XX

PA

Antibodies specific for PRO polype

The growth of tumors in mammals, if

PI polypeptide activity or expression

XX

Claim 61; Fig 18; 226pp; English.

XX

The present invention describes an occupation of generation of ge CC The present invention describes an antibody that binds to a human CC protein (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1790; CC PRO3434; PRO1927; PRO3567; PRO1293; PRO1293; PRO1393; PRO4344; PRO4354; CC PRO4397; PRO4079; PRO1555; PRO1295; PRO1293; PRO1393; PRO4344; PRO4354; CC anticancer activity and can be used to diagnose tumours in mammals, by CC detecting complex formation when the antibody is contacted with test CC cells. Increased expression of genes encoding (I) can also be detected CC to diagnose tumours. Agents which inhibit the activity of (I), CC especially the antibodies, or an atisense oligonucleotide which CC hybridises to genes encoding (I), can be used to inhibit tumour growth, CC preferably by inducing cell death. Methods from the present invention CC can be used to identify compounds which inhibit the biological activity CC of (I). AAC58019 to AAC58102 represent PCR primers and hybridisation CC probes used in examples from the present invention for human PRO CC sequences. AAC58103 to AAC58122 and AAB24021 to AAB24040 represent human CC PRO polynucleotide and protein sequences given in the exemplification of the present invention for human PRO CC protes used in examples from the present invention for human PRO CC protes used in examples from the present invention for human PRO CC protes used in examples from the present invention for human PRO CC protein sequences given in the exemplification of the present invention for human PRO CC protein sequences given in the exemplification of the present invention for human PRO CC protein sequences given in the exemplification of the present invention for human PRO CC protein sequences given in the present invention for human PRO CC protein sequences given in the present human PRO CC protein sequences given in the exemplification of the present invention for human PRO CC protein sequences given in the present invention for human PRO CC protein sequences given in the protein sequences given in the protein sequences given in the protein s

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alignment_block:
                                                          alignment_scores:
US-09-684-016-48411 x AAB24029
                             Percent Similarity:
                                                Quality:
                                      Ratio:
                             53.00
2.650
71.429
                              Percent
                             Identity:
                              42
                              28
0
.857
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38 GACCTAATGGCGCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGT

Align seg 1/1

to: AAB24029 from: 1

to:

180

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AC AAB43274 standard; Protein; 601 AA
AC AAB43274;

AC AAB43274;

AC AAB43274;

AC AAB43274;

AC AAB43274;

AC AAB43274;

AC AAB43274;

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AC AAB43274;

AC AAC7446 to AAC77606 encode the presences have activitless such as: CC antiinflammatory; antibacterial; antiing composition of pathological conditions associated conditions associated conditions associated composition of pathological conditions associated composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of composition of compositi
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                                        antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antitinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The nucleic acids can be used to express OREX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritts; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID, AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal hæmoglobinuria; burn; wound; pone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 5260-5262; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF3038 polypeptide sequence SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:AAB43274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    open reading frame; ORFX; detection;
        neurodegenerative disorders, osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic; hepatotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus arythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived polypeptides, for treatment of use and identification of therapeutic agents
                                                                                                                                                                                                 New nucleic acid sequences expressed in uterine cancer tissues, derived polypeptides, for treatment of uterine and endometrial of
                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                            WPI; 1999-591957/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DE19817948-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endometrium; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human endometrium tumour EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY60285 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              384
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                                                                                                                                                                                                                                                                                                                                                                       Rosenthal A,
                                                                                                                                                                                                                                                                                                                                                                                                                             (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treatment; uterine;
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52:174
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anticancer and

This invention describes novel human nucleic acid (cDNA) sequences that are highly expressed in uterine tumour tissue and which have

cytostatic activity. (A) are used (i) for recombinant

Claim 23; Page 412; 444pp; German.

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seq_documentation_block:
ID AAW20131 standard; Pr
XX AAW20131;
XX O8-JUL-1997 (first e
XX Cytoplasmic; vaccine;
KW Cytoplasmic; vaccine;
KW binding compound; bac
KW duodenal ulcer diseas
XX duodenal ulcer pylori.
XX Key Locat
FT Misc-difference 8
FT Misc-1996: 96WO-1
XX WO9640893-A1.
XX PD 19-DEC-1996: 95US-(
PR 07-JUN-1995; 95US-(
PR 07-JUN-1995; 95US-(
PR 07-JUN-1995; 95US-(
PR 07-JUN-1995; 95US-(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of polypeptides (B) and (ii) to isolate complete genes. (B) are used (1) to identify agents suitable for treatment of uterine or endometrial cancer; (ii) directly for treating these forms of cancer (including expression from gene therapy vectors) and (iii) for generation of specific antibodies. (A) are identified by assembling ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H. pylori cell envelope transporter protein 13726562.aa
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95US-0487032
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seq_name:
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US-09-684-016-48411/rev x AAW20131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transporter protein.

C transporter protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, infection or to identify H. pylori life cycle activators or inhibitors. C useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55679) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                         Cytoplasmic; vaccine; prevention; identification; binding compound; bacteria; inhibitor; duodenal ulce
                                                                                                                                                                                                                                                                                                                      H. pylori transporter protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                                                             Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  172 yGlnLysIleAlaLeuIleGlyHisSerGlyCysGlyLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCTCGCATTGCGCCATTAGGTCATCATCATGGTTAAGGCATCT:::::||||||||
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                                                                   96US-0630405
95US-0487032
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2.684
61.290
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                                                                                                                                                                                                                                                            duodenal ulcer
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                                                                                                                                                                                                                                                           bacterium;
er disease;
                                                                                                                                                                                                                                                                                          treatment; infection; envelope;
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0
38.710
                                                                                                                                                                                                                                                           life cycle; activa chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186
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Smith D,

Mellgaerd

BL;

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DR WPI, 1997-052306/05.

DR WPSDB, AAT67872.

XX

PH Helicobacter pylori nucleic acid sequences and related prolipeptide(g) - useful for vaccines to treat or prevent H. pylori prolipeptide, and to detect Helicobacter

XX

XX

This sequence represents a H. pylori transporter protein.

CC This protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

CC The protein may be used in a vaccine to prevent or treat H. pylori or treat H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

CC The protein may be used find a vaccine to prevent or treat H. pylori polypeptide binding compounds, the sequence of H. pylori life cycle activators or inhibitors.

CC The protein may be used for ORR of at least 180 nucleotides, useful as potential H. pylori life cycle activators or inhibitors.

CC The protein predicted from vaccine development, the amino condition of the predicted from vaccine development, the amino condition of the sequences of interest, particular regions can be condition, e.g. in E. coli hosts.

XX

Sequence 377 AA;

alignment_scores:

Duality: 51.00

Percent Similarity: 61.290 Percent Identity: 38.710

Percent Similarity: 61.290 Percent Identity: 38.710

Percent Similarity: 61.290 Percent Identity: 38.710

Percent Similarity: 10.290 Percent Identity: 38.710

Percent Similarity: 61.290 Percent Identity:
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Database sequences: 21225;
Database length: 22503292
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Query length: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM of: US-09-684-016-48411 to:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
                                 cgn2_6/ptodata/2/iaa/6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -Q=/Cgn2_1/USPTO_Spool/US09684016/runat_19032002_084440_20900/app_query.fasta_1.182
-QB=!ESUMEd_Patents_AA .QPMT=fastan -SUFFIX-std rai
-GAPOP-12.000 -GAPOXT-4.000 -MINMATCH+0.100 -XCAOPCL-0.000
-LOODEXT=0.000 -GAPOXT-4.500 -GGAPOXT-0.050 -XCAOPOP-10.000
-XGAPEXT=0.500 -FGAPOP-4.500 -FGAPEXT=7.000 -YGAPOP-10.000
-YGAPOXT-0.500 -FGAPOX-6.000 -FGAPOXT-7.000 -YGAPOP-10.000
-YGAPOXT-0.500 -DELOP-6.000 -FGAPOXT-7.000 -YGAPOX-10.000
-YGAPOXT-0.500 -DELOP-6.000 -DELOXT-7.000 -YGAPOX-10.000
-THR_SCORE-PCT -THR_MAX=100 -THR_MIN-0 -ALIGN-45 -MODE=LOCAL
-OUTFMT-pfs -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09684016_@CGNI_1_0 -NCPU=6 -ICPU=3 -LONGLOG
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; Sequence 4, Application US/09085199B
; Patent No. 6235879
                                                      seq_name:
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                                                                                                                                                                                                                                                                                                                                                          US-08-762-428A-6
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alignment_scores:
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-345-212-14-

/cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-09-249-003-14-

/cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-374-483-2+

/cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-374-483-5+
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ye, usually applicant: Breslow, Esther M. APPLICANT: Meister, Alton APPLICANT: Meister, Alton APPLICANT: Meister, Alton APPLICANT: Meister, Alton APPLICANT: Meister, Alton APPLICANT: Meister, Alton APPLICANT: Meister, Alton Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant Applicant A
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ATTORNEY/AGENT INFORMATION:
NAME: TIMIAN, SUSAN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            |||||||:::|||:::|||::: ||| || || || |||||:::||| 231
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MEDIUM TYPE: Floppy disk
                                                                                 231 gGlyHisThrAlaCysAlaAspAlaTyrLeuThrProThr 244
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                                                                                                                                                              42 AGGTCATCAGGGTTGTAAGGCATCTCACATTTACAATACC
                                                                                                                                                                                                                                                                                                                             86 CATGTGAAACTTACCAGTCAGTGCAGCCCT.....CGCATTGCGCCATT 43
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TELEPHONE: 716-263-1600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-085-199B-4
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5. 6120993
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Ratio:
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Gaps: 1
Percent Identity: 40.000
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US-09-085-199B-4
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TELEFAX: (970) 668-2052

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 914
TYPP
Sequence 5, Application US/09085199B Patent No. 6235879 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Kb storage
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: MS DOS 5.0
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ADDRESSEE: Oppedahl & Larson
STREET: PO Box 5270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: LATSON, MARINA T.
REGISTRATION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UBS
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                 /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-085-199B-5
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Ratio:
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Chopra, Vikramjit Singh
Kalchman, Michael
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68.421
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seq_documentation_block:
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US-09-684-016-48411/rev x US-09-085-1998-5
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   Quality:
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; OTHER INFORMATION:
US-09-085-1998-5
                                                                                                   seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-549-515-9
                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-09-085-199B-5 from: 1 to:
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                    Sequence 9, Application US/08549515 Patent No. 6054123
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (970) 668-2052 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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HYPOTHETICAL: no
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Larson, Marina T.
REGISTACION NUMBER: 32038
REFERENCE/DOCKET NUMBER: UB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                          271 yGlnCys.....ArgLeuAlaProLeuIleGlnValIleLeuAspCysS 286
                                                                                                                                                                                                                                                                                                         255 ValPheAsnSerLeuAspMetSerArgSerValSerValThrAlaAlaGl 271
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APPLICANT:
                                                                                                                                            286 erHisLeuTyrAsp 290
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                                                                                                                                                                19 CTCACATTTACAAT 6
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APPLICANT: Kalchman, Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS
SOFTWARE: WordPerfect
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: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chopra, Vikramjit Singh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayden. Michael R.
Hackam, Abigail
Huq, A.H.M. Mahbubul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.00
2.077
68.421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Huntington-interacting protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBC.P-013US2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.842
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TITLE OF INVENTION:

Dimethylsulphoxide Reductase Enzyme

Haemophilus Influenzae

Klein, Michel H

Loosmore, Sheena M

NUMBER OF SEQUENCES: 1

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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                             seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-866-545-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                             Sequence 4, Application US/08866545 Patent No. 6265535 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                 119 rLysGlyHisMetThrLysCysAspGlyCysTyrAsp 131
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LENGTH: 207 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                             103 ArgTyrCysHisMetAlaCysProTyrGlyAlaProGlnTyrAsnGluTh 119
                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                      44 .....ATGGCGCAATGCGAGGGCTGCACTGAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTA.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 27-OCT-1995
                  STREET:
                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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New York
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Suite 701, 330 Unviersity Avenue
            Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                    Takasaki,
                                                                                                                                                                                           Murali,
                                                                                                                                                                                                         Greene, Mark I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canada
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3.400
51.724
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                                                                         ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR USES
27
                                                                                                                                                    PEPTIDES AND PEPTIDE
                                                                                                                                                                        Wataru
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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-866-545-4
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                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                        Sequence 11, Application US/08232087A Patent No. 5866372
                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stein, Harald
APPLICANT: Drkop, Horst
APPLICANT: Latza, Ute
TITLE OF INVENTION: Lymphoid CD30-Antigen
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                 60 uAlaCys 62
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REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 30-MA
                                                                                                         STATE: Virginia
                                                                                                                           CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                         ZIP:
                                                                                        COUNTRY:
                                                                                                                                                           ADDRESSEE:
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                                                                         22042
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                                                                                                                                        E: Birch, Stewart, Kolasch & Birch, LLP
8110 Gatehouse Road, Suite 500 East
                                                                                  U.S.A.
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4.167
63.158
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: 36.842
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-684-016-48411 x US-08-232-087A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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LENGTH: 159 amin
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: DOS
                                                                                                                                                                                                                                                          APPLICANT: NAGATA, Shiqekazu
APPLICANT: ITOH, Naoto
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
NUMBER OF SEQUENCES: 11
                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyHisCysGl 93
                                                                                                                                                                                             ADDRESSEE: James W. Hellwege STREET: P.O. Box 2266 Eads Station CITY: Arlington.
                                                                                                                                                COUNTRY: U
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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APPLICATION NUMBER: FILING DATE: 28-MA
                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1..159
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Protein
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TELEFAX: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Murphy Jr., Gerald M. REGISTRATION NUMBER: 28,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Ratio:
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                                                                                                                                                                                   Virginia
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3.846
65.000
28-MAR-1994
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             US/08/219,237B
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35.000
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seq_documentation_block:
; Sequence 15, Applicati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-477-347-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
NAME: James W. Hellwege
REGISTRATION NUMBER: 28,808
REFERENCE/DOCKET NUMBER: 51
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: APPLICANT:
                             APPLICATION NUMBER: IL 10
FILING DATE: 08-JUL-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: APPLICANT:
                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 uAlaCys 95
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                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
NAME: Townsend, G. F
REGISTRATION NUMBER:
                                                                                                     FILING DATE:
                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                STREET: 419 Sever CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                    20004
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BIGDA, Jacek
BELETSKY, Igor
                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                    419 Seventh Street, N.W.
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                                                                                                                                                                                                                                                                            Floppy disk
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4.167
63.158
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                  G. Kevin
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                                                                     IL 106271
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                                                                                                                       08/115,685
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Gaps: 0
Percent Identity: 36.842
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-477-347-15
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US-09-684-016-48411 x US-08-477-347-15
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Percent Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 159 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: METT, IGOR
APPLICANT: ENGELMANN, Hartmut
TITLE OF INVENTION: THE INHIBITORS
                  PRIOR APPLICATION DATA:
                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BIGDA, Jacek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-628-5197
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TELEFAX: 248633
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                                                                                                                                                                                                 APPLICATION NUMBER: US/0: FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 419 Seven
 APPLICATION NUMBER:
                                                                                       APPLICATION NUMBER: IL 99 FILING DATE: 06-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uAlaCys 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                    20004
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                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BELETSKY, Igor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WALLACH, David
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linear
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4.167
63.158
                                                                                                      IL 94039
                                                                                                                                                                                                                                   US/08/476,862
IL 90339
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Gaps: 0
Percent Identity: 36.842
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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-08-468-560C-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08468560C Patent No. 6270998
TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ITOH, NAOTO
APPLICANT: YONEHARA, S
TITLE OF INVENTION: DN
TITLE OF INVENTION: AN
                                      REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                              APPLICATION NUMBER: US/08/4
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/468,560C
                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NAGATA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 GGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 uAlaCys 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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4.167
63.158
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Gaps: 0
Percent Identity: 36.842
                                                                             20-4393P
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TYPE: amino acid STRANDEDNESS: si

single

amino acids

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alignment_scores:
Quality:
Ratio:
                                                                                     ; TOPOLOGY: 1; MOLECULE TYPE: US-08-974-022-50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-974-022-50
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                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: OSTEOPROTEGERIN NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Boyle, Willaim J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 uAlaCys 95
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                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 12-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                              LENGTH:
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5. 6015938
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                                                                                                                                                            amino acid
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                                                                                                                                                                       224 amino acids
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Gaps: 0
Percent Identity: 36.842
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Gaps:
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alignment_block:
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                                                                     Align seg 1/1 to: US-08-795-445A-50
                                                                                                         US-09-684-016-48411 x US-08-795-445A-50
                                                                                                                                                              Percent Similarity:
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 50
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TOPOLOGY: line
MOLECULE TYPE: 1
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STATE: California
107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
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APPLICATION NUMBER: (
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Chang, Ming-Shi
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                                8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/795,445A
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                                                                                                                                                                                                                                                                                                                                              : 224 amino acids amino acid
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linear
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    Sequence 50, Applicati
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                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-974-186-50
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                                                                 Sequence 50, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
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LENGTH: 224 amino acid
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       APPLICANT:
                                                                                                                                                                                                  123 uAlaCys 125
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T: One Amgen Center Drive
Thousand Oaks
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Lacey, David L.
Calzone, Frank J
Chang, Ming-Shi
Boyle, Willaim J.
Lacey, David L.
Calzone, Frank J.
Chang, Ming-Shi
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Gaps: 0
Percent Identity: 36.842
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US-08-974-186-50
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                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                             Sequence 50,
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SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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STATE: California
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                     NUMBER OF SEQUENCES:
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7TP: 91320-1789
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REFERENCE/DOCKET NUMBER: A
REFERENCE/DOCKET NUMBER: A
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                                     ZIP: 91320-1789
                                                 COUNTRY:
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1840 Dehavilland Drive
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Lacey, David L.
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alignment_block:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5948641
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                   APPLICATION NUMBER: US FILING DATE: Herewith CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                       SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
NFORMATION FOR SEQ ID NO: 50:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: METAL RESPONSE ELEMENT BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 GGGCTGC 64
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                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/795,446B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                                                                         3174 Porter Drive
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                                                                                                                                                                                        IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
                                                                                            Herewith
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4.167
63.158
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                                                                                                             US/08/864,804
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36.842
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seq_documentation_block:
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US-08-864-804-1
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           ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE UTTACE.
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                               SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 TyrCysTyrCysGlyGlyProGlyGluTrpAsnLeuLysMetLeuGlnCy 205
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IMMEDIATE SOURCE:
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                                                             FILING DATE: DE CLASSIFICATION:
                                                                                                                              FILING DATE: May-30-97 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                          APPLICATION NUMBER:
                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                               FILING DATE: May-29-98
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STRANDEDNESS: si
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REFERENCE/DOCKET
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9410 KEY WEST AVENUE
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SYSTEM: PC-DOS/MS-DOS
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NUMBER:
                                                                                                                                                                                                                                US/09/086,483A
                                                                                                                                                                                                                                                             Release #1.0, Version
                                                                                                                                                                 60/050,936
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39.130
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-086-483A-4
; MOLECULE TYPE: protein US-09-041-886-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09041886
                                                                            TELEPHONE: (619) 535-901
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (301) 309-8439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tent No.
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 427 amino acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 uAlaCys 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GGGCTGC 64
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CITY: San Diego
STATE: California
                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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Gaps: 0
Percent Identity: 36.842
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alignment_block:
US-09-684-016-48411 x US-09-006-353A-5
                                                                                                                                                     ; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-006-353A-5
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US-09-684-016-48411 x US-09-041-886-2
                                                                                                    alignment_scores:
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                                                      Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09006353A Patent No. 6261801
                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 uAlaCys 125
                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                     LENGTH:
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RUBEN, STEVEN
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YU, GUO-LIANG
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63.158
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Gaps: 0
Percent Identity: 36.842
                                                    Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                             PF341
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                                                                                       Length:
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36.842
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Align seg 1/1 to: US-09-006-353A-5 from: 1 to: 427

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alignment_block:
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; MOLECULE TYPE:
US-08-553-436A-8
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                                                                               Align seg 1/1
                                                                                                                   US-09-684-016-48411/rev x US-08-553-436A-8
                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08553436A Patent No. 5866790
                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (212) 382-088
TELEX: 236925
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: HESSE, Holger
APPLICANT: MULLER-ROBER, Bernd
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
TITLE OF INVENTION: CONCENTRATION
399 GluAspLysTyrHisPheSerCysGlnPheSerAlaAspLeuMetAlaMe 415
                                SEQUENCE CHARACTERISTICS LENGTH: 766 amino acid
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE P
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 CysArgCysAlaTyrGlyTyrTyrGlnAspGluThrThrGlyArgCysGl 123
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REFERENCE/DOCKET NUMBER: P/951-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/553,436A FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                               to: US-08-553-436A-8
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1180 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 382-0700
                                                                                                                                                                                                                                                                                                                    protein
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24-MAY-1993
                                                                                                                                                                            50.00
2.273
38.596
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                                                                                                                                                                              Percent Identity:
                                                                               from: 1
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26.316
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 5620000;
GENERAL INFORMATION:
GENERAL TOANT: DEAN, JURRIEN
CONT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08453472 Patent No. 5626846
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,462
                                                                                                                        TOPOLOGY: unknown MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 26-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: TITLE OF INVENTION:
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                                                                                                      ORGANISM:
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                TELEX: 421792
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/364,379 FILING DATE: 12-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/038,948 FILING DATE: 26-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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CELL TYPE:
                  TISSUE TYPE:
                                                     DEVELOPMENTAL
                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                                                                                               LENGTH:
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                                                                                                        mouse
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                                                                                                                                                                                                                                                                                                   (212) 758-4800
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BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
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ORGANELLE

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seq_documentation_block:
; Sequence 7, Applicatio
; Patent No. 5641487
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US-09-684-016-48411 x US-08-453-472-6
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    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DEAN, JURRIEN
                                                                                        FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 9915
TELECOMMUNICATION INFORMATION:
                  TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                         FILING DATE: 20-AUG-1992
PRIOR APPLICATION UDATA:
APPLICATION UNMBER: US 07/364,379
FILING DATE: 12-JUN-1989
                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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SEQUENCE CHARACTERISTICS:
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NAME/KEY:
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                                   TELEPHONE: (202)
TELEFAX: (202)
TELEX: 6714627
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 26-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-038-948-7
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1100 New York Avenue, N.W.
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                                                     (202) 861-3000
02) 822-0944
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2.553
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Gaps: 2
Percent Identity: 34.211
                                                                                                             99152/E-266-88/2
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-038-948-8
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US-09-684-016-48411 x US-08-038-948-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
    Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-08-038-948-7 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08038948 Patent No. 5641487
                                                                                                                                                                                                APPLICATION NUMBER: US/08/038,948
FILING DATE: 26-MAR-1993
CLASSIFICATION: 435
CRISCIPLICATION DATA:
APPLICATION NUMBER: US 07/930,462
FILING DATE: 20-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
TELEPHONE: (202) 861-31
TELEFAX: (202) 822-094
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: DEAN,
                                                                             ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 99152/E-266-88/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As 368
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TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alTyrSerHisGln 379
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Percent Identity: 34.211
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-038-948-8
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US-09-684-016-48411 x US-08-038-948-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10,
                                                                                              APPLICATION NUMBER: US 07/364,379
FILING DATE: 12-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: SCOTT, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: 99152/E-266-88/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEPAX: (202) 822-0944
                                     TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION: APPLICANT: DEAN,
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ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/930,462 FILING DATE: 20-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CONTRACEPTIVE VACCINE BASED ON TITLE OF INVENTION: ALLOIMMUNIZATION WITH ZONA PELLUCIDA POLYPEPTIDES
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375 alTyrSerHisGln 379
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                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
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                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/038,948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-038-948-10
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713 amino acids
nino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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34.211
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; STRANDEDNESS:
; TOPOLOGY: lir
; MOLECULE TYPE:
US-08-038-948-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-453-952-6
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DEAN, JUITITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                      REFERENCE/DOCKET NUMBER: 20 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       APPLICATION NUMBER: US 0 FILING DATE: 20-AUG-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 01 FILING DATE: 26-MAR-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
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                                                                                                                                                                   APPLICATION NUMBER: US 07/364,379 FILING DATE: 12-JUN-1989
                                   TELEFAX:
                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 30-May
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: NEW YORK
STATE: NEW YORK
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                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 PARK AVENUE
                                   : (212) 758-4800
(212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEAN, JURRIEN
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                                                                                                            36,434
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                                                                                            2026-4032 US
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2
34.211
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SEQUENCE CHARACTERISTICS:

ENGTH:

amino acid

STRANDEDNESS: TOPOLOGY: un

unknown

single

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seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-862-903-6
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                sq_documentation_block:
Sequence 6, Application US/08862903
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: 0
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 pGlyPheMetAspPhe....
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                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 TTTATTCCACACAA 121
                                                                                                                                                                                        STREET: 345 PA
CITY: NEW YORK
STATE: NEW YOR
CLASSIFICATION:
                              APPLICATION NUMBER: US/08/862,903
                                                                                                                                                         ZIP: 10154
                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                        NEW YORK
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                  30-May-1995
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BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
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Gaps: 2
Percent Identity: 34.211
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; IDENTIFICATION METHOD: ; OTHER INFORMATION: mol US-08-862-903-6
                                                                                                         seq_documentation_block:
                                                                                                                                            seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-549-515-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                     Sequence 6, Application US/08549515 Patent No. 6054123
                  GENERAL INFORMATION:
APPLICANT: Loosmo
APPLICANT: Klein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
APPLICANT: Loosmore, Sheena APPLICANT: Klein, Michel H TITLE OF INVENTION: Haemoph
                                                                                                                                                                                                                108 TTTATTCCACACAA 121
                                                                                                                                                                                                                                                      368 pGlyPheMetAspPhe......GluV 375
                                                                                                                                                                                                                                                                                                                           353 CysHisCysGluSerProValSerIleAspGluLeuCysAlaGln...As 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                              375 alTyrSerHisGln 379
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       58 GGCCTGCACTGACTGGTAAGTTTCACATGTAAGGTGATACTTATCTTCAA 107
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212
TELEX: 421792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 12-JUN-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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                                                                                                                                                                                                                                                                                                                                                               TGTAAATGTGAGATGCCTTACAACCCTGATGACCTAATGGCGCAATGCGA 57
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212) 751-6849
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                                 Sheena M
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Gaps: 2
Percent Identity: 34.211
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Haemophilus Influenzae

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alignment_block: US-09-684-016-48411 x US-08-549-515-6
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                                                                                                                                                                                                                                                                                        Sequence 12, Application US/08549515 Patent No. 6054123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                    APPLICANT: LOOSMORE, Sheena M
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Haemophilu
TITLE OF INVENTION: Dimethylsu
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 27-OCT-1995 CLASSIFICATION: 536 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 ArgTyrCysHisMetAlaCysProTyrAspAlaProGlnTyrAspAlaGl 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AGGTATTGTAAATGTGAGATGCCTTACAACCCTGATGACCTA.....
   COMPUTER:
                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                    кк: Canada
м5G 1R7
                                                                                                        Toronto
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                                                                                         Ontario
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                                                                                                                         Suite 701,
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Suite 701, 330 Unviersity Avenue
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IBM PC compatible
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3.429
51.852
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                                                                                                                                                                                                  Dimethylsulphoxide Reductase Enzyme
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                                                                                                                         330 Unviersity Avenue
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Percent Identity:
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alignment_block:
US-09-684-016-48411 x US-08-549-515-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            STREET:
STREET:
Rahway
CITY: Rahway
CITY: New Jersey
GI.S.A.
                                  APPLICATION NUMBER: US/0:
FILING DATE: 25-MAY-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wallen, John W.
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cully, Doris F.
APPLICANT: Arena, Joseph P.
APPLICANT: Liu, Ken K.
APPLICANT: Vassilatis, Demetrics
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
TITLE OF INVENTION: CHANNELS
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LENGTH: 205 amino acids
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NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,515
FILING DATE: 27-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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REGISTRATION NUMBER:
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3.429
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  NUMBER:
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n Release #1.0, Version #1.30
                                                                                                                                                      Release #1.0, Version #1.25
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                                                                                                                US/08/249,112
                35,403
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Gaps:
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TELECOMMUNICATION INFORMATION:

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alignment_scores:
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                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/249,11:
FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN, John W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908) 594-4720
NFORMATION FOR SEQ ID NO: 4
                                       TELEFAX: (908) 594-47
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         documentation_block:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Liu, Ken K.
APPLICANT: Vassilatis, Demetrios
TITLE OF INVENTION: DNA ENCODING GLUTAMATE GATED CHLORIDE
TITLE OF INVENTION: CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LysIleLeuTyrSerSerArgIleSerLeuThrSerSerCysProMetAr 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 07065
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                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US95/06556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Wallen, John W.
126 E. Lincoln Ave., P.O. Box 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arena,
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-06556-4
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US-09-684-016-48411/rev x PCT-US95-06556-4
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7
Patent No.
                                                                                TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                              REFERENCE/DOCKET NUMBER: SF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0)
FILING DATE: 09-JAN-1998
ATTORNEY_AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lebecque,
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               TOPOLOGY:
                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Palo Alto
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                                                                LENGTH:
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5. 6271014
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TN NO: 7:
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peptide
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NUMBER OF SEQUENCES:

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alignment_scores:
Quality:
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                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-357-598-12
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US-09-684-016-48411 x US-09-115-954-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-115-954-4
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APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30409
CURRENT APPLICATION NUMBER: US/09/115,954B
CURRENT FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
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                                                                                        Sequence 12, Application US/08357598 Patent No. 5705625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 4, Application US/09115954B Patent No. 6200776
      GENERAL INFORMATION:
APPLICANT: Civin, (
APPLICANT: Small, I
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Boron, Walter F
APPLICANT: Bril, Antoine M
APPLICANT: Khandoudi, Nassirah
APPLICANT: Martin, Xavier
                                                                                                                                                                                                                 305 TyrCysArgCysThrLeuProGluAsnProAsnAsn 316
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Donald

NOVEL PROTEIN TYROSINE KINASE, JAK3
                                                 Curt I.
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Percent Identity:
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-357-598-12
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                                                                                                                                                                                                                                  Sequence 12, Application US/09003289 Patent No. 5916792
                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                   APPLICANT: Civin, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL I
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/37,598
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/03:
                                                                                                                                                                                                                                                                                                                                            340 euSerHis 342
                                                                                                                                                                                                                                                                                                                                                                                                                    323 uGlyProAspTyrLysGlyCysLeuIleArgProGlyPheLeuValGlyL 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 619/678-5070 TELEFAX: 619/678-5099
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ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                      STREET:
                                                      STATE:
                                                                       CITY:
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                                  COUNTRY:
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                                                                                                         ADDRESSEE:
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92037
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SYSTEM: PC-DOS/MS-DOS
                                                                                                         Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
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2.400
55.556
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                                                                                                                                                            NOVEL PROTEIN TYROSINE KINASE,
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Gaps: 2
Percent Identity: 38.889
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alignment_block:
US-09-684-016-48411/rev x US-09-003-289-12
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 846 amino acids
                                                                                                                                                                                                                                                                                                                                              quence 12, Application PC/TUS9516435 ENERAL INFORMATION:
              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3 NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                   STREET: **-
STREET: ta Jolla
CITY: La Jolla
TTATE: CA
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 euSerHis 342
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
  APPLICATION NUMBER:
                                                                                                                                                              COUNTRY:
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REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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15-DEC-1994
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PCT/US95/16435
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Gaps: 2
Percent Identity: 38.889
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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-09-115-954-8
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PCT-US95-16435-12
     Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                              SEQ ID NO 8
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                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: EP97401714.7
EARLIER FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/115,954B CURRENT FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                          APPLICANT: Rawlings, Christopher J
APPLICANT: Doe, Trudy R
TITLE OF INVENTION: NOVER COMPOUNDS
FILE REFERENCE: GH-30409
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                                                                                                                                                                                                               SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Martin, Xavier
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Khandoudi, Nassirah
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                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 AspAspSerPheLeuLeuThrCys......ValGlnProLe 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TCGCATTGCGCCATTAGGTCATCAGGGTTGTAAGGCA 21
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Ratio:
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619/678-5099
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     48.00
4.800
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Length: 12
Gaps: 0
Percent Identity: 50.000
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seq_documentation_block:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-115-954-2
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US-09-684-016-48411 x US-09-115-954-8
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/09352990 Patent No. 6255090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
                                                                                                                APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetase
FILE REFERENCE: BB-1191
CURRENT APPLICATION NUMBER: US/09/352,990
CURRENT FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092,866
EARLIER FILING DATE: July 15, 1998
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                                                                                 SOFTWARE: Microsoft Office 97
                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/115,954B CURRENT FILING DATE: 1998-07-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL COMPOUNDS FILE REFERENCE: GH-30409
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APPLICANT: Bril, Antoine M
ORGANISM: Glycine max
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                                       ENGTH:
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5. 6200776
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; MOLECULE TYPE: US-08-445-586-9
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US-09-684-016-48411/rev x US-09-352-990-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-445-586-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                     TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 26-AUG-1993
APPLICATION NUMBER: UP 236
FILING DATE: 28-AUG-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                     LENGTH:
TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Bone-Related Sulfatase-Like
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                                     TOPOLOGY:
                                                                                                                                                                            REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 02
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                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9, Application US/08445586
5. 5627050
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                                                   amino acid
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                                                                    583 amino acids
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1300 I Street, N.W.
                                                                                                                          202-408-4400
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                                                                                                                                            202-408-4000
                  peptide
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03-DEC-1992
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; MOLECULE TYPE: US-08-484-493-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/08484493 Patent No. 5728381
                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERRNGE/DOCKET NUMBER: 8416:
TELECOMMUNICATION INFORMATION:
TELECHONE: 516,742-343
                                                                                                                             TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,493
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acid
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                 STRANDEDNESS:
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                                   TOPOLOGY:
                                                                                                                                                                 TELEFAX: 516-742-4366
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Clements, Peter R
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Anson, Donald S
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                                   linear
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               protein
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Gaps: 0
Percent Identity: 41.176
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-484-494-14
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; Sequence 14, Applicati
; Patent No. 5798239
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                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/484,494
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Didigilo, Frank S
REGISTRATION UMBER: 31,346
REFERENCE/DOCKET NUMBER: 8416Z
TELEPHONE: 516-742-4443
                                                                                                                            TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acids
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                                                                                                                                                 TELEPHONE: 516-742-4366
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    STRANDEDNESS:
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STATE: New York
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Anson, Donald S
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Clements, Peter R
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                                       linear
                protein
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3.357
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Gaps: 0
Percent Identity: 41.176
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alignment_scores:
 Quality:

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; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-345-212-14
                                                                              alignment_scores:
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US-09-684-016-48411/rev x US-08-484-494-14
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                              Ratio:
Percent Similarity:
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14,
                                                                                                                                                                                                                            TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 991,973
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIG19110, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 84162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 400 CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                           LENGTH:
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                                                               Quality:
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                                                                                                                                                                                          H: 583 amino acids amino acid
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5932211
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Occhiodoro, Teresa
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Anson, Donald S
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17
Gaps: 0
Percent Identity: 41.176
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Percent Identity: 41.176
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alignment_block:
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; MOLECULE TYPE:
US-09-249-003-14
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US-09-684-016-48411/rev x US-08-345-212-14
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                                   Percent Similarity:
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                                                                                                                                                                                                                                                                    TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991
APPLICATION NUMBER: 17-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO, Frank S
REGISTRATION NUMBER: 31,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 583 amino acid
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                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: HOPWOOD, JOHN J
TITLE OF INVENTION: GLYCOSYLATION VARIANT.
TITLE OF INVENTION: IDURONATE 2-SULFATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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TELEPHONE: 516-742-4366
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REFERENCE/DOCKET NUMBER: 8416Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Clements, Peter R
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Anson, Donald S
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                                 Percent Identity: 41.176
                                                                  Length:
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Align seg 1/1 to: US-09-249-003-14

from: 1

. 6 US-09-684-016-48411/rev x US-09-249-003-14

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alignment_scores:
Quality:
Ratio:
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; LOCATION: 1831..4290
; OTHER INFORMATION: /n
US-08-374-483-2
                                                                                                                                       alignment_block:
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                                                                                Align seg 1/1 to: US-08-374-483-2
                                                                                                                   US-09-684-016-48411 x US-08-374-483-2
                                                                                                                                                                        Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GEORGE, SAMUEL E.
APPLICANT: BLAZING, MICHAEL A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 ThrProAsnPheAsnProValGlySerAsnGlyCysPheAlaThrHisVa 486
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                       FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
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CITY: ARLINGTON
STATE: VIRGINIA
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                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 820 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                        linear
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                                                                                                                                                                        Percent Identity: 40.000
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; NAME/KEY:
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US-08-374-483-5
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                                                                                                                                          Align seg 1/1 to: US-08-374-483-5 from: 1
                                                                                                                                                                                                                                   Percent Similarity:
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TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                        372 CysSerGlnProTyrProSerGlyAspSerCysCysAlaGluProProAl 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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APPLICANT: BLAZING, MICHAEL A.
TITLE OF INVENTION: ADENOVIRAL VECTOR SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                    49 GCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGTA 88
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                                                                                                       49 GCAATGCGAGGGCTGCACTGACTGGTAAGTTTCACATGTA 88
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1 CLASSIFICATION:
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Quality:
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1100 NORTH GLEBE ROAD, 8TH FLOOR
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SYSTEM: PC-DOS/MS-DOS
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